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(21) International Application Number: PCT/US99/18298		(72) Inventors: JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). McCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LaVALLIE, Edward, R.; 133 Ann Lee Road, Harvard, MA 01451 (US). COLLINS-RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). EVANS, Cheryl; 18801 Bent Willow Circle, Germantown, MA 20874 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 12 Foxrock Court, Dublin 4 (IE). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US). STEININGER, Robert, J., II; 100 Reed Street, Cambridge, MA 02140 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). WONG, Gordon, G.; 239 Clark Road, Brookline, MA 02146 (US). CLARK, Hilary, F.; 495 Harkness Avenue, San Francisco, CA 94134 (US). FECHTEL, Kim; 46 Marion Road, Arlington, MA 02174 (US).	
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(71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US).			
(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM			
(57) Abstract			
Novel polynucleotides and the proteins encoded thereby are disclosed.			

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SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

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This application is a continuation-in-part of the following applications:

- (1) provisional application Ser. No. 60/096,622 (GI 6075), filed August 14, 1998;
 - (2) provisional application Ser. No. 60/096,815 (GI 6076), filed August 17, 1998;
 - (3) provisional application Ser. No. 60/099,229 (GI 6077), filed September 4, 1998;
 - 15 (4) provisional application Ser. No. 60/105,368 (GI 6078), filed October 23, 1998;
 - (5) provisional application Ser. No. 60/115,234 (GI 6079), filed January 8, 1999;
 - (6) provisional application Ser. No. 60/119,931 (GI 6080), filed February 12, 1999;
 - (7) provisional application Ser. No. 60/120,575 (GI 6081), filed February 18, 1999;
 - (8) provisional application Ser. No. 60/132,020 (GI 6082), filed April 30, 1999;
 - 20 (9) provisional application Ser. No. 60/XXX,XXX (GI 6083), filed August 11, 1999;
- all of which are incorporated by reference herein.

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FIELD OF THE INVENTION

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

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BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the
5 past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which
10 isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the
15 cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 821;
- 25 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 120 to nucleotide 821;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 1 to nucleotide 1625;
- (e) a polynucleotide comprising the nucleotide sequence of the full-
30 length protein coding sequence of clone co62_12 deposited under accession number ATCC 98825;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;

- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone co62_12 deposited under accession number ATCC 98825;
- 5 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- 10 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 15 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:1.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 821; the nucleotide sequence of SEQ ID NO:1 from nucleotide 120 to nucleotide 821; the nucleotide sequence of SEQ ID NO:1 from nucleotide 1 to nucleotide 1625; the nucleotide sequence of the full-length protein coding sequence of clone co62_12 deposited under accession number ATCC 98825; or the
- 25 nucleotide sequence of a mature protein coding sequence of clone co62_12 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone co62_12 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein
- 30 comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having

biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(ab) the nucleotide sequence of the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(bb) the nucleotide sequence of the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to

a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 821, and extending
5 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 821, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 821. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
10 NO:1 from nucleotide 120 to nucleotide 821, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 120 to nucleotide 821, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 120 to nucleotide 821. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 1 to nucleotide 1625, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 1 to nucleotide 1625, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 1 to nucleotide 1625.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:2;
- (b) a fragment of the amino acid sequence of SEQ ID NO:2, the
25 fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
co62_12 deposited under accession number ATCC 98825;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 9 to nucleotide 1013;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 96 to nucleotide 1013;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone lo311_8 deposited under accession number ATCC 98825;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone lo311_8 deposited under accession number ATCC 98825;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 9 to nucleotide 1013; the nucleotide sequence of SEQ ID NO:3 from nucleotide 96 to nucleotide 1013; the nucleotide sequence of the full-length protein coding sequence of clone lo311_8 deposited under accession number ATCC 98825; or the
5 nucleotide sequence of a mature protein coding sequence of clone lo311_8 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825. In further preferred
10 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 162
15 to amino acid 171 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and
 - (ab) the nucleotide sequence of the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 9 to nucleotide 1013, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 9 to nucleotide 1013, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 9 to nucleotide 1013. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 96 to nucleotide 1013, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 96 to nucleotide 1013, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 96 to nucleotide 1013.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30 (a) the amino acid sequence of SEQ ID NO:4;

(b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ
10 ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 162 to amino acid 171 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 352 to nucleotide 825;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ns197_1 deposited under accession number ATCC 98825;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ns197_1 deposited under accession number ATCC 98825;
- 25 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (h) a polynucleotide encoding a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 352 to nucleotide 825; the nucleotide sequence of the full-length
10 protein coding sequence of clone ns197_1 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone ns197_1 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825. In further preferred
15 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having
20 biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(ab) the nucleotide sequence of the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(bb) the nucleotide sequence of the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending
20 contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 352 to nucleotide 825, and extending
25 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 352 to nucleotide 825, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 352 to nucleotide 825.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ
10 ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 86 to nucleotide 829;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 149 to nucleotide 829;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pj193_5 deposited under accession
20 number ATCC 98825;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pj193_5 deposited under accession number ATCC 98825;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
25 protein coding sequence of clone pj193_5 deposited under accession number ATCC 98825;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pj193_5 deposited under accession number ATCC 98825;
- (h) a polynucleotide encoding a protein comprising the amino acid
30 sequence of SEQ ID NO:8;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 86 to nucleotide 829; the nucleotide sequence of SEQ ID NO:7 from nucleotide 149 to nucleotide 829; the nucleotide sequence of the full-length protein coding sequence of clone pj193_5 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone pj193_5 deposited
15 under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pj193_5 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological
20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 119 to amino acid 128 of SEQ ID NO:8.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

- (ab) the nucleotide sequence of the cDNA insert of clone pj193_5 deposited under accession number ATCC 98825;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 pj193_5 deposited under accession number ATCC 98825;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated
- 25 according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 86 to nucleotide 829, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 86 to nucleotide 829, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 86 to
- 30 nucleotide 829. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 149 to nucleotide 829, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from

nucleotide 149 to nucleotide 829, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 149 to nucleotide 829.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
- (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

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pj193_5 deposited under accession number ATCC 98825;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably

15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 119 to amino acid 128 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an

20 isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 174 to nucleotide 1292;

25

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pj317_2 deposited under accession number ATCC 98825;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pj317_2 deposited under accession number ATCC 98825;

30

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pj317_2 deposited under accession number ATCC 98825;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pj317_2 deposited under accession number ATCC 98825;

- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:9.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 174 to nucleotide 1292; the nucleotide sequence of the full-length protein coding sequence of clone pj317_2 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone pj317_2 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pj317_2 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 181 to amino acid 190 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(ab) the nucleotide sequence of the cDNA insert of clone pj317_2 deposited under accession number ATCC 98825;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(bb) the nucleotide sequence of the cDNA insert of clone pj317_2 deposited under accession number ATCC 98825;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 174 to nucleotide 1292, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 174 to nucleotide 1292, to a nucleotide sequence

corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 174 to nucleotide 1292.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

10 pj317_2 deposited under accession number ATCC 98825;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably

15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 181 to amino acid 190 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an

20 isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 7 to nucleotide 2517;

25 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 904 to nucleotide 2517;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pt332_1 deposited under accession number ATCC 98825;

30 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pt332_1 deposited under accession number ATCC 98825;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any
15 one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:11.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 7 to nucleotide 2517; the nucleotide sequence of SEQ ID NO:11 from nucleotide 904 to nucleotide 2517; the nucleotide sequence of the full-length protein
20 coding sequence of clone pt332_1 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone pt332_1 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825. In further preferred
25 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having
30 biological activity, the fragment comprising the amino acid sequence from amino acid 413 to amino acid 422 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(ab) the nucleotide sequence of the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(bb) the nucleotide sequence of the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 7 to nucleotide

2517, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 7 to nucleotide 2517, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 7 to nucleotide 2517. Also preferably the polynucleotide isolated according to the above
5 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 904 to nucleotide 2517, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 904 to nucleotide 2517, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 904 to nucleotide 2517.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
- (b) a fragment of the amino acid sequence of SEQ ID NO:12, the
15 fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred
20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence
25 from amino acid 413 to amino acid 422 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:13 from nucleotide 18 to nucleotide 257;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qc297_15 deposited under accession number ATCC 98825;

- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qc297_15 deposited under accession number ATCC 98825;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 18 to nucleotide 257; the nucleotide sequence of the full-length protein coding sequence of clone qc297_15 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone qc297_15 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having

biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:13, but excluding the poly(A) tail at the
3' end of SEQ ID NO:13; and

(ab) the nucleotide sequence of the cDNA insert of clone
qc297_15 deposited under accession number ATCC 98825;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:13, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:13; and

(bb) the nucleotide sequence of the cDNA insert of clone
qc297_15 deposited under accession number ATCC 98825;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 18 to nucleotide 257, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 18 to nucleotide 257, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 18 to nucleotide 257.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
- (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 21 to nucleotide 2432;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qg596_12 deposited under accession number ATCC 98825;

- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qg596_12 deposited under accession number ATCC 98825;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qg596_12 deposited under accession number ATCC 98825;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qg596_12 deposited under accession number ATCC 98825;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:15.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 21 to nucleotide 2432; the nucleotide sequence of the full-length protein coding sequence of clone qg596_12 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone qg596_12 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qg596_12 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having

biological activity, the fragment comprising the amino acid sequence from amino acid 397 to amino acid 406 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:15, but excluding the poly(A) tail at the
3' end of SEQ ID NO:15; and

(ab) the nucleotide sequence of the cDNA insert of clone
qg596_12 deposited under accession number ATCC 98825;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:15, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:15; and

(bb) the nucleotide sequence of the cDNA insert of clone
qg596_12 deposited under accession number ATCC 98825;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 21 to nucleotide 2432, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 21 to nucleotide 2432, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 21 to nucleotide 2432.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
- (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qg596_12 deposited under accession number ATCC 98825;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 397 to amino acid 406 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 339 to nucleotide 2105;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 501 to nucleotide 2105;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rb649_3 deposited under accession number ATCC 98825;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rb649_3 deposited under accession number ATCC 98825;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 339 to nucleotide 2105; the nucleotide sequence of SEQ ID NO:17 from nucleotide 501 to nucleotide 2105; the nucleotide sequence of the full-length protein coding sequence of clone rb649_3 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone rb649_3 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological

activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 289 to amino acid 298 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 15 (aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and
 - (ab) the nucleotide sequence of the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
 - 25 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and
 - 30 (bb) the nucleotide sequence of the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 339 to nucleotide 2105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 339 to nucleotide 2105, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 339 to nucleotide 2105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 501 to nucleotide 2105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from
15 nucleotide 501 to nucleotide 2105, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 501 to nucleotide 2105.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:18;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 289 to amino acid 298 of SEQ ID NO:18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 509 to nucleotide 2467;
- 5 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ca106_19x deposited under accession number ATCC 98835;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;
- 10 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ca106_19x deposited under accession number ATCC 98835;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;
- 15 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 509 to nucleotide 2467; the nucleotide sequence of the full-length protein coding sequence of clone ca106_19x deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone ca106_19x deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert

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of clone ca106_19x deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 321 to amino acid 330 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and
 - (bb) the nucleotide sequence of the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 509 to nucleotide 2467, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 509 to nucleotide 2467, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide
- 15 509 to nucleotide 2467.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
 - 20 (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;
- the protein being substantially free from other mammalian proteins. Preferably such
- 25 protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ
- 30 ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 321 to amino acid 330 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 179 to nucleotide 802;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 242 to nucleotide 802;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ci52_2 deposited under accession number ATCC 98835;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ci52_2 deposited under accession number ATCC 98835;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:21.
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Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 179 to nucleotide 802; the nucleotide sequence of SEQ ID NO:21 from nucleotide 242 to nucleotide 802; the nucleotide sequence of the full-length protein coding sequence of clone ci52_2 deposited under accession number ATCC 98835; or the

nucleotide sequence of a mature protein coding sequence of clone ci52_2 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

- (ab) the nucleotide sequence of the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

- (bb) the nucleotide sequence of the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 179 to nucleotide 802, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 179 to nucleotide 802, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 179 to nucleotide 802. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 242 to nucleotide 802, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 242 to nucleotide 802, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 242 to nucleotide 802.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
- (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:22.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 46 to nucleotide 714;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 538 to nucleotide 714;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone md124_16 deposited under accession
15 number ATCC 98835;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone md124_16 deposited under accession number ATCC 98835;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone md124_16 deposited under accession number
20 ATCC 98835;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone md124_16 deposited under accession number ATCC 98835;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;
- 25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 46 to nucleotide 714; the nucleotide sequence of SEQ ID NO:23 from nucleotide 538 to nucleotide 714; the nucleotide sequence of the full-length protein coding sequence of clone md124_16 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone md124_16 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone md124_16 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 106 to amino acid 115 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and
 - (ab) the nucleotide sequence of the cDNA insert of clone md124_16 deposited under accession number ATCC 98835;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone md124_16 deposited under accession number ATCC 98835;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 46 to nucleotide 714, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 46 to nucleotide 714, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 46 to nucleotide 714. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 538 to nucleotide 714, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 538 to nucleotide 714, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 538 to nucleotide 714.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

- (b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and
- (c) the amino acid sequence encoded by the cDNA insert of clone md124_16 deposited under accession number ATCC 98835;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 106 to amino acid 115 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 92 to nucleotide 1726;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:25 from nucleotide 1211 to nucleotide 1726;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pk366_7 deposited under accession number ATCC 98835;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone pk366_7 deposited under accession number ATCC 98835;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pk366_7 deposited under accession number ATCC 98835;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone pk366_7 deposited under accession number ATCC 98835;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 92 to nucleotide 1726; the nucleotide sequence of SEQ ID NO:25 from nucleotide 1211 to nucleotide 1726; the nucleotide sequence of the full-length protein coding sequence of clone pk366_7 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone pk366_7 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pk366_7 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 267 to amino acid 276 of SEQ ID NO:26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and
- (ab) the nucleotide sequence of the cDNA insert of clone pk366_7 deposited under accession number ATCC 98835;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 pk366_7 deposited under accession number ATCC 98835;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 92 to nucleotide 1726, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 92 to nucleotide 1726, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide

92 to nucleotide 1726. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 1211 to nucleotide 1726, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from
5 nucleotide 1211 to nucleotide 1726, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 1211 to nucleotide 1726.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:26;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pk366_7 deposited under accession number ATCC 98835;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 267 to amino acid 276 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 16 to nucleotide 1788;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:27 from nucleotide 61 to nucleotide 1788;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pl741_5 deposited under accession number ATCC 98835;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pl741_5 deposited under accession number ATCC 98835;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:27.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 16 to nucleotide 1788; the nucleotide sequence of SEQ ID NO:27 from nucleotide 61 to nucleotide 1788; the nucleotide sequence of the full-length protein coding sequence of clone pl741_5 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone pl741_5 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having

biological activity, the fragment comprising the amino acid sequence from amino acid 290 to amino acid 299 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:27, but excluding the poly(A) tail at the
3' end of SEQ ID NO:27; and

(ab) the nucleotide sequence of the cDNA insert of clone
pl741_5 deposited under accession number ATCC 98835;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:27, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:27; and

(bb) the nucleotide sequence of the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 16 to nucleotide 1788, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 16 to nucleotide 1788, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 16 to nucleotide 1788. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 61 to nucleotide 1788, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 61 to nucleotide 1788, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 61 to nucleotide 1788.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
- (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 290 to amino acid 299 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 629 to nucleotide 2338;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pp314_19 deposited under accession number ATCC 98835;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pp314_19 deposited under accession number ATCC 98835;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- 15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 20 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:29.
- 25

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 629 to nucleotide 2338; the nucleotide sequence of the full-length protein coding sequence of clone pp314_19 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone pp314_19 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

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comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(ab) the nucleotide sequence of the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(bb) the nucleotide sequence of the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 629 to nucleotide 2338, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 629 to nucleotide 2338, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 629 to nucleotide 2338.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 158 to nucleotide 1102;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pv35_1 deposited under accession number ATCC 98835;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pv35_1 deposited under accession number ATCC 98835;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment
- 15 comprising eight contiguous amino acids of SEQ ID NO:32;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:31.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 158 to nucleotide 1102; the nucleotide sequence of the full-length protein coding sequence of clone pv35_1 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone pv35_1 deposited under accession number ATCC 98835. In other preferred embodiments, the
- 30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 152 to amino acid 161 of SEQ ID NO:32.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and
 - (bb) the nucleotide sequence of the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 158 to nucleotide 1102, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 158 to nucleotide 1102, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 158 to nucleotide 1102.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:32;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 152 to amino acid 161 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 413 to nucleotide 733;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pw337_6 deposited under accession number ATCC 98835;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pw337_6 deposited under accession number ATCC 98835;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;
- 15 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:33.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 413 to nucleotide 733; the nucleotide sequence of the full-length protein coding sequence of clone pw337_6 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone pw337_6 deposited under accession number ATCC 98835. In other preferred embodiments, the
- 30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:34.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
 - 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and
 - (bb) the nucleotide sequence of the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 413 to nucleotide 733, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 413 to nucleotide 733, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 413 to nucleotide 733.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:34;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 678 to nucleotide 938;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rd610_1 deposited under accession number ATCC 98835;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rd610_1 deposited under accession number ATCC 98835;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:35.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 678 to nucleotide 938; the nucleotide sequence of the full-length protein coding sequence of clone rd610_1 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone rd610_1 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:36.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and
 - (bb) the nucleotide sequence of the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 678 to nucleotide 938, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 678 to nucleotide 938, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 678 to nucleotide 938.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:36;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 75 to nucleotide 494;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 447 to nucleotide 494;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rd810_6 deposited under accession number ATCC 98835;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rd810_6 deposited under accession number ATCC 98835;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rd810_6 deposited under accession number ATCC 98835;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rd810_6 deposited under accession number ATCC 98835;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:37.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 75 to nucleotide 494; the nucleotide sequence of SEQ ID NO:37 from nucleotide 447 to nucleotide 494; the nucleotide sequence of the full-length protein coding sequence of clone rd810_6 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone rd810_6 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rd810_6 deposited under accession number ATCC 98835. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding
5 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:37, but excluding the poly(A) tail at the
3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone
rd810_6 deposited under accession number ATCC 98835;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

30 (ba) SEQ ID NO:37, but excluding the poly(A) tail at the
3' end of SEQ ID NO:37; and

(bb) the nucleotide sequence of the cDNA insert of clone
rd810_6 deposited under accession number ATCC 98835;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 75 to nucleotide
10 494, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 75 to nucleotide 494, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 75 to nucleotide 494. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:37 from nucleotide 447 to nucleotide 494, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 447 to nucleotide 494, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 447 to nucleotide 494.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
- (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
25 (c) the amino acid sequence encoded by the cDNA insert of clone rd810_6 deposited under accession number ATCC 98835;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 181 to nucleotide 1080;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cf85_1 deposited under accession number ATCC 98850;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cf85_1 deposited under accession number ATCC 98850;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- (h) a polynucleotide encoding a protein comprising a fragment of the
20 amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein
25 of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
30 25% of the length of SEQ ID NO:39.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 181 to nucleotide 1080; the nucleotide sequence of the full-length protein coding sequence of clone cf85_1 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone cf85_1 deposited

under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein
5 comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 145
10 to amino acid 154 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 20 (aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and
- (ab) the nucleotide sequence of the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

- (bb) the nucleotide sequence of the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 181 to nucleotide 1080, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 181 to nucleotide 1080, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 181 to nucleotide 1080.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
- (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 145 to amino acid 154 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 161 to nucleotide 1348;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 599 to nucleotide 1348;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd504_18 deposited under accession number ATCC 98850;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd504_18 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 161 to nucleotide 1348; the nucleotide sequence of SEQ ID NO:41

from nucleotide 599 to nucleotide 1348; the nucleotide sequence of the full-length protein coding sequence of clone dd504_18 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone dd504_18 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 193 to amino acid 202 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and
 - (ab) the nucleotide sequence of the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and
- (bb) the nucleotide sequence of the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;
- 5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 161 to nucleotide 1348, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 161 to nucleotide 1348, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 161 to nucleotide 1348. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 599 to nucleotide 1348, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 599 to nucleotide 1348, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 599 to nucleotide 1348.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
- (b) a fragment of the amino acid sequence of SEQ ID NO:42, the
30 fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 193 to amino acid 202 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 70 to nucleotide 1386;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone np26_3 deposited under accession number ATCC 98850;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone np26_3 deposited under accession number ATCC 98850;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone np26_3 deposited under accession number ATCC 98850;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone np26_3 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 70 to nucleotide 1386; the nucleotide sequence of the full-length protein coding sequence of clone np26_3 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone np26_3 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone np26_3 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 214 to amino acid 223 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(ab) the nucleotide sequence of the cDNA insert of clone np26_3 deposited under accession number ATCC 98850;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(bb) the nucleotide sequence of the cDNA insert of clone np26_3 deposited under accession number ATCC 98850;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 70 to nucleotide
20 1386, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 70 to nucleotide 1386, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 70 to nucleotide 1386.

In other embodiments, the present invention provides a composition comprising
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone np26_3 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence
5 from amino acid 214 to amino acid 223 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 60 to nucleotide 3515;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm412_12 deposited under accession number ATCC 98850;
- 15 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm412_12 deposited under accession number ATCC 98850;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- (h) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein
30 of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 60 to nucleotide 3515; the nucleotide sequence of the full-length protein coding sequence of clone pm412_12 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone pm412_12 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 571 to amino acid 580 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(ab) the nucleotide sequence of the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(bb) the nucleotide sequence of the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 60 to nucleotide
20 3515, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 60 to nucleotide 3515, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 60 to nucleotide 3515.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:46;

(b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence
5 from amino acid 571 to amino acid 580 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 1490 to nucleotide 1780;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 1556 to nucleotide 1780;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm421_3 deposited under accession
15 number ATCC 98850;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
20 protein coding sequence of clone pm421_3 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850;
- (h) a polynucleotide encoding a protein comprising the amino acid
25 sequence of SEQ ID NO:48;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 1490 to nucleotide 1780; the nucleotide sequence of SEQ ID NO:47 from nucleotide 1556 to nucleotide 1780; the nucleotide sequence of the full-length protein coding sequence of clone pm421_3 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone pm421_3 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and
 - (ab) the nucleotide sequence of the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(bb) the nucleotide sequence of the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 1490 to nucleotide 1780, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 1490 to nucleotide 1780, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 1490 to nucleotide 1780. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 1556 to nucleotide 1780, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 1556 to nucleotide 1780, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 1556 to nucleotide 1780.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:48;

- (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 64 to nucleotide 486;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:49 from nucleotide 217 to nucleotide 486;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pv6_1 deposited under accession number ATCC 98850;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone pv6_1 deposited under accession number ATCC 98850;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pv6_1 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone pv6_1 deposited under accession number ATCC 98850;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 64 to nucleotide 486; the nucleotide sequence of SEQ ID NO:49 from nucleotide 217 to nucleotide 486; the nucleotide sequence of the full-length protein coding sequence of clone pv6_1 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone pv6_1 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pv6_1 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and
- (ab) the nucleotide sequence of the cDNA insert of clone pv6_1 deposited under accession number ATCC 98850;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 pv6_1 deposited under accession number ATCC 98850;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 64 to nucleotide 486, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 64 to nucleotide 486, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide

64 to nucleotide 486. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 217 to nucleotide 486, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 217 to nucleotide 486, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 217 to nucleotide 486.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:50;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pv6_1 deposited under accession number ATCC 98850;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 379 to nucleotide 3783;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 460 to nucleotide 3783;
- 30 (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 1983 to nucleotide 3938;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qs14_3 deposited under accession number ATCC 98850;
- 5 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qs14_3 deposited under accession number ATCC 98850;
- 10 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;
- 15 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:51.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 379 to nucleotide 3783; the nucleotide sequence of SEQ ID NO:51 from nucleotide 460 to nucleotide 3783; the nucleotide sequence of SEQ ID NO:51 from nucleotide 1983 to nucleotide 3938; the nucleotide sequence of the full-length protein coding sequence of clone qs14_3 deposited under accession number ATCC 98850; or the
- 30 nucleotide sequence of a mature protein coding sequence of clone qs14_3 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino

acid sequence of SEQ ID NO:52 from amino acid 536 to amino acid 1135. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty,
5 most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 562 to amino acid 571 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
10 ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
20 qs14_3 deposited under accession number ATCC 98850;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 25 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:51, but excluding the poly(A) tail at the
30 3' end of SEQ ID NO:51; and
 - (bb) the nucleotide sequence of the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 379 to nucleotide 3783, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 379 to nucleotide 3783, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide
- 15 379 to nucleotide 3783. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 460 to nucleotide 3783, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 460 to nucleotide 3783, to a nucleotide sequence corresponding to the 3' end
- 20 of said sequence of SEQ ID NO:51 from nucleotide 460 to nucleotide 3783. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 1983 to nucleotide 3938, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 1983 to nucleotide 3938,
- 25 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 1983 to nucleotide 3938.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 30
- (a) the amino acid sequence of SEQ ID NO:52;
 - (b) the amino acid sequence of SEQ ID NO:52 from amino acid 536 to amino acid 1135;
 - (c) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and

(d) the amino acid sequence encoded by the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52 or the amino acid sequence of SEQ ID NO:52 from amino acid 536 to amino acid 1135. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 562 to amino acid 571 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 1 to nucleotide 843;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 469 to nucleotide 843;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qy338_9 deposited under accession number ATCC 98850;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qy338_9 deposited under accession number ATCC 98850;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qy338_9 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qy338_9 deposited under accession number ATCC 98850;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:53.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 1 to nucleotide 843; the nucleotide sequence of SEQ ID NO:53 from nucleotide 469 to nucleotide 843; the nucleotide sequence of the full-length protein coding sequence of clone qy338_9 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone qy338_9 deposited
15 under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qy338_9 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological
20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 135 to amino acid 144 of SEQ ID NO:54.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

- (ab) the nucleotide sequence of the cDNA insert of clone qy338_9 deposited under accession number ATCC 98850;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 qy338_9 deposited under accession number ATCC 98850;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 1 to nucleotide 843, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 1 to nucleotide 843, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide
- 30 1 to nucleotide 843. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 469 to nucleotide 843, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from

nucleotide 469 to nucleotide 843, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 469 to nucleotide 843.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:54;
- (b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

10 qy338_9 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably

15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 135 to amino acid 144 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an

20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 283 to nucleotide 906;
- 25 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 906;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rc58_1 deposited under accession number ATCC 98850;
- 30 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rc58_1 deposited under accession number ATCC 98850;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:55.
- 15

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 283 to nucleotide 906; the nucleotide sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 906; the nucleotide sequence of the full-length protein coding sequence of clone rc58_1 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone rc58_1 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:56.

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Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and
 - (ab) the nucleotide sequence of the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and
 - (bb) the nucleotide sequence of the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 283 to nucleotide

906, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 283 to nucleotide 906, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 283 to nucleotide 906. Also preferably the polynucleotide isolated according to the above
5 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 906, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 906, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 906.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:56;
- (b) a fragment of the amino acid sequence of SEQ ID NO:56, the
15 fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
- (c) the amino acid sequence encoded by the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred
20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence
25 from amino acid 99 to amino acid 108 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:57 from nucleotide 56 to nucleotide 973;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rd232_5 deposited under accession number ATCC 98850;

- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rd232_5 deposited under accession number ATCC 98850;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:57.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 973; the nucleotide sequence of the full-length protein coding sequence of clone rd232_5 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone rd232_5 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having

biological activity, the fragment comprising the amino acid sequence from amino acid 148 to amino acid 157 of SEQ ID NO:58.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:57.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:57, but excluding the poly(A) tail at the
3' end of SEQ ID NO:57; and

(ab) the nucleotide sequence of the cDNA insert of clone
rd232_5 deposited under accession number ATCC 98850;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:57, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:57; and

(bb) the nucleotide sequence of the cDNA insert of clone
rd232_5 deposited under accession number ATCC 98850;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 973, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 973, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 973.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;
- (b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
- (c) the amino acid sequence encoded by the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 148 to amino acid 157 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 893 to nucleotide 2596;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ck213_12 deposited under accession number ATCC 98918;

- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ck213_12 deposited under accession number ATCC 98918;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:59.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 893 to nucleotide 2596; the nucleotide sequence of the full-length protein coding sequence of clone ck213_12 deposited under accession number ATCC 98918; or the nucleotide sequence of a mature protein coding sequence of clone ck213_12 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having

biological activity, the fragment comprising the amino acid sequence from amino acid 279 to amino acid 288 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 10 (aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;
 - 15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- 20 (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
 - (bb) the nucleotide sequence of the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - 30 (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 893 to nucleotide 2596, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 893 to nucleotide 2596, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 893 to nucleotide 2596.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
- (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 279 to amino acid 288 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 29 to nucleotide 1750;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pg195_1 deposited under accession number ATCC 98918;

- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pg195_1 deposited under accession number ATCC 98918;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:62;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 29 to nucleotide 1750; the nucleotide sequence of the full-length protein coding sequence of clone pg195_1 deposited under accession number ATCC 98918; or the nucleotide sequence of a mature protein coding sequence of clone pg195_1 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having

biological activity, the fragment comprising the amino acid sequence from amino acid 282 to amino acid 291 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:61, but excluding the poly(A) tail at the
3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone
pg195_1 deposited under accession number ATCC 98918;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(bb) the nucleotide sequence of the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 29 to nucleotide 1750, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 29 to nucleotide 1750, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 29 to nucleotide 1750.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:62;
- (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 282 to amino acid 291 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 1147 to nucleotide 1440;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 1234 to nucleotide 1440;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pw460_5 deposited under accession number ATCC 98918;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pw460_5 deposited under accession number ATCC 98918;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:63.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 1147 to nucleotide 1440; the nucleotide sequence of SEQ ID NO:63 from nucleotide 1234 to nucleotide 1440; the nucleotide sequence of the full-length protein coding sequence of clone pw460_5 deposited under accession number ATCC 98918; or the nucleotide sequence of a mature protein coding sequence of clone pw460_5 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological

activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 44
5 to amino acid 53 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:63.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 15 (aa) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and
 - (ab) the nucleotide sequence of the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
25 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
30 pw460_5 deposited under accession number ATCC 98918;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 1147 to nucleotide 1440, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 1147 to nucleotide 1440, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 1147 to nucleotide 1440. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 1234 to nucleotide 1440, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from
15 nucleotide 1234 to nucleotide 1440, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 1234 to nucleotide 1440.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:64;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 46 to nucleotide 1356;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 127 to nucleotide 1356;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qa136_1 deposited under accession number ATCC 98918;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qa136_1 deposited under accession number ATCC 98918;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:65.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 46 to nucleotide 1356; the nucleotide sequence of SEQ ID NO:65 from nucleotide 127 to nucleotide 1356; the nucleotide sequence of the full-length protein coding sequence of clone qa136_1 deposited under accession number ATCC 98918; or the

nucleotide sequence of a mature protein coding sequence of clone qa136_1 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918. In further preferred
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a polynucleotide encoding
10 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 213 to amino acid 222 of SEQ ID NO:66.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced
15 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:65; and

(ab) the nucleotide sequence of the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:65; and

(bb) the nucleotide sequence of the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65. Also preferably the polynucleotide isolated according to the above process comprises a
- 10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 46 to nucleotide 1356, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 46 to nucleotide 1356, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 46 to nucleotide 1356. Also preferably the polynucleotide
- 15 isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 127 to nucleotide 1356, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 127 to nucleotide 1356, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide
- 20 127 to nucleotide 1356.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;

the protein being substantially free from other mammalian proteins. Preferably such

30 protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 213 to amino acid 222 of SEQ ID NO:66.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 206 to nucleotide 1624;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:67 from nucleotide 542 to nucleotide 1624;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qy1261_2 deposited under accession number ATCC 98918;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qy1261_2 deposited under accession number ATCC 98918;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone qy1261_2 deposited under accession number ATCC 98918;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:68;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:67.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 206 to nucleotide 1624; the nucleotide sequence of SEQ ID NO:67 from nucleotide 542 to nucleotide 1624; the nucleotide sequence of the full-length protein coding sequence of clone qy1261_2 deposited under accession number ATCC 98918; or
5 the nucleotide sequence of a mature protein coding sequence of clone qy1261_2 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918. In further preferred
10 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having
15 biological activity, the fragment comprising the amino acid sequence from amino acid 231 to amino acid 240 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (aa) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and
 - (ab) the nucleotide sequence of the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

(bb) the nucleotide sequence of the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 206 to nucleotide 1624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 206 to nucleotide 1624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 206 to nucleotide 1624. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 542 to nucleotide 1624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 542 to nucleotide 1624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 542 to nucleotide 1624.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:68;

(b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and

(c) the amino acid sequence encoded by the cDNA insert of clone
gy1261_2 deposited under accession number ATCC 98918;
the protein being substantially free from other mammalian proteins. Preferably such
protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the
amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably
comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ
ID NO:68 having biological activity, the fragment comprising the amino acid sequence
10 from amino acid 231 to amino acid 240 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an
isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:69;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:69 from nucleotide 1359 to nucleotide 1817;
- (c) a polynucleotide comprising the nucleotide sequence of the full-
length protein coding sequence of clone rd432_4 deposited under accession
number ATCC 98918;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the
cDNA insert of clone rd432_4 deposited under accession number ATCC 98918;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
protein coding sequence of clone rd432_4 deposited under accession number
ATCC 98918;
- 25 (f) a polynucleotide encoding a mature protein encoded by the cDNA
insert of clone rd432_4 deposited under accession number ATCC 98918;
- (g) a polynucleotide encoding a protein comprising the amino acid
sequence of SEQ ID NO:70;
- (h) a polynucleotide encoding a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:70 having biological activity, the fragment
comprising eight contiguous amino acids of SEQ ID NO:70;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of
(a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:69.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 1359 to nucleotide 1817; the nucleotide sequence of the full-length
10 protein coding sequence of clone rd432_4 deposited under accession number ATCC 98918; or the nucleotide sequence of a mature protein coding sequence of clone rd432_4 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918. In further preferred
15 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having
20 biological activity, the fragment comprising the amino acid sequence from amino acid 71 to amino acid 80 of SEQ ID NO:70.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:69.

Further embodiments of the invention provide isolated polynucleotides produced
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

(ab) the nucleotide sequence of the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

(bb) the nucleotide sequence of the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 1359 to nucleotide
25 1817, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 1359 to nucleotide 1817, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 1359 to nucleotide 1817.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:70;

(b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence
10 from amino acid 71 to amino acid 80 of SEQ ID NO:70.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 884 to nucleotide 1195;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 947 to nucleotide 1195;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rb789_14 deposited under accession
20 number ATCC 207004;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rb789_14 deposited under accession number ATCC 207004;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
25 protein coding sequence of clone rb789_14 deposited under accession number ATCC 207004;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rb789_14 deposited under accession number ATCC 207004;
- (h) a polynucleotide encoding a protein comprising the amino acid
30 sequence of SEQ ID NO:72;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:71.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 884 to nucleotide 1195; the nucleotide sequence of SEQ ID NO:71 from nucleotide 947 to nucleotide 1195; the nucleotide sequence of the full-length protein coding sequence of clone rb789_14 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone rb789_14 deposited
15 under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rb789_14 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological
20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:72.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

- (ab) the nucleotide sequence of the cDNA insert of clone rb789_14 deposited under accession number ATCC 207004;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 rb789_14 deposited under accession number ATCC 207004;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 884 to nucleotide 1195, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 884 to nucleotide 1195, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide
- 30 884 to nucleotide 1195. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 947 to nucleotide 1195, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from

nucleotide 947 to nucleotide 1195, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 947 to nucleotide 1195.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:72;
- (b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

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rb789_14 deposited under accession number ATCC 207004;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably

15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an

20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73;
 - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 69 to nucleotide 374;
 - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 25 NO:73 from nucleotide 186 to nucleotide 374;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd137_1 deposited under accession number ATCC 207004;
 - (e) a polynucleotide encoding the full-length protein encoded by the
- 30 cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd137_1 deposited under accession number ATCC 207004;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:73.
- 15

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 69 to nucleotide 374; the nucleotide sequence of SEQ ID NO:73 from nucleotide 186 to nucleotide 374; the nucleotide sequence of the full-length protein coding sequence of clone yd137_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yd137_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004. In further preferred

20

25 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having

30 biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:74.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:73.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and
 - (bb) the nucleotide sequence of the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 69 to nucleotide

374, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 69 to nucleotide 374, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 69 to nucleotide 374. Also preferably the polynucleotide isolated according to the above
5 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 186 to nucleotide 374, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 186 to nucleotide 374, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 186 to nucleotide 374.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- (b) a fragment of the amino acid sequence of SEQ ID NO:74, the
15 fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:74. In further preferred
20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence
25 from amino acid 46 to amino acid 55 of SEQ ID NO:74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:75 from nucleotide 8 to nucleotide 343;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 50 to nucleotide 343;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd218_1 deposited under accession number ATCC 207004;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd218_1 deposited under accession number ATCC 207004;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 8 to nucleotide 343; the nucleotide sequence of SEQ ID NO:75 from nucleotide 50 to nucleotide 343; the nucleotide sequence of the full-length protein coding sequence of clone yd218_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yd218_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological

activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 15 (aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
 - 25 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
 - 30 yd218_1 deposited under accession number ATCC 207004;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 8 to nucleotide 343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 8 to nucleotide 343, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 8 to nucleotide 343. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 50 to nucleotide 343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from
15 nucleotide 50 to nucleotide 343, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 50 to nucleotide 343.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:76;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 84 to nucleotide 1679;
- 5 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye11_1 deposited under accession number ATCC 207004;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye11_1 deposited under accession number ATCC 207004;
- 10 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye11_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye11_1 deposited under accession number ATCC 207004;
- 15 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:77.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 84 to nucleotide 1679; the nucleotide sequence of the full-length protein coding sequence of clone ye11_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone ye11_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert

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of clone ye11_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 261 to amino acid 270 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(ab) the nucleotide sequence of the cDNA insert of clone ye11_1 deposited under accession number ATCC 207004;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(bb) the nucleotide sequence of the cDNA insert of clone ye11_1 deposited under accession number ATCC 207004;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 84 to nucleotide 1679, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 84 to nucleotide 1679, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide
- 15 84 to nucleotide 1679.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- 20 (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ye11_1 deposited under accession number ATCC 207004;

- the protein being substantially free from other mammalian proteins. Preferably such
- 25 protein comprises the amino acid sequence of SEQ ID NO:78. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ
- 30 ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 261 to amino acid 270 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 72 to nucleotide 1646;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 180 to nucleotide 1646;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye72_1 deposited under accession number ATCC 207004;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye72_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye72_1 deposited under accession number ATCC 207004;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye72_1 deposited under accession number ATCC 207004;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 72 to nucleotide 1646; the nucleotide sequence of SEQ ID NO:79 from nucleotide 180 to nucleotide 1646; the nucleotide sequence of the full-length protein coding sequence of clone ye72_1 deposited under accession number ATCC 207004; or the

nucleotide sequence of a mature protein coding sequence of clone ye72_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye72_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 257 to amino acid 266 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

- (ab) the nucleotide sequence of the cDNA insert of clone ye72_1 deposited under accession number ATCC 207004;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

- (bb) the nucleotide sequence of the cDNA insert of clone ye72_1 deposited under accession number ATCC 207004;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 72 to nucleotide 1646, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 72 to nucleotide 1646, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 72 to nucleotide 1646. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 180 to nucleotide 1646, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 180 to nucleotide 1646, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 180 to nucleotide 1646.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 25 (a) the amino acid sequence of SEQ ID NO:80;
- (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ye72_1 deposited under accession number ATCC 207004;
- 30

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 257 to amino acid 266 of SEQ ID NO:80.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 954 to nucleotide 2423;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 1224 to nucleotide 2423;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye78_1 deposited under accession number ATCC 207004;
- 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye78_1 deposited under accession number ATCC 207004;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:82;
- 25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:81.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:81 from nucleotide 954 to nucleotide 2423; the nucleotide sequence of SEQ ID NO:81 from nucleotide 1224 to nucleotide 2423; the nucleotide sequence of the full-length protein coding sequence of clone ye78_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone ye78_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ ID NO:82.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:81.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(bb) the nucleotide sequence of the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:81 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 954 to nucleotide 2423, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 954 to nucleotide 2423, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 954 to nucleotide 2423. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 1224 to nucleotide 2423, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 1224 to nucleotide 2423, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 1224 to nucleotide 2423.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:82;

- (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:82, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ ID NO:82.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 176 to nucleotide 1321;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:83 from nucleotide 233 to nucleotide 1321;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye90_1 deposited under accession number ATCC 207004;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye90_1 deposited under accession number ATCC 207004;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone ye90_1 deposited under accession number ATCC 207004;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:84;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:83.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:83 from nucleotide 176 to nucleotide 1321; the nucleotide sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1321; the nucleotide sequence of the full-length protein coding sequence of clone ye90_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone ye90_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 186 to amino acid 195 of SEQ ID NO:84.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:83.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and
 - (bb) the nucleotide sequence of the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:83 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 176 to nucleotide 1321, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 176 to nucleotide 1321, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide

176 to nucleotide 1321. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1321, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from
5 nucleotide 233 to nucleotide 1321, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1321.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:84;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:84. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:84, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 186 to amino acid 195 of SEQ ID NO:84.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 105 to nucleotide 605;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yi62_1 deposited under accession number
30 ATCC 207004;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yi62_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:86;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:85.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:85 from nucleotide 105 to nucleotide 605; the nucleotide sequence of the full-length protein coding sequence of clone yi62_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yi62_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:86.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:85.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:85, but excluding the poly(A) tail at the
- 10 3' end of SEQ ID NO:85; and
- (ab) the nucleotide sequence of the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 yi62_1 deposited under accession number ATCC 207004;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:85 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 105 to nucleotide 605, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 105 to nucleotide 605, to a nucleotide
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 105 to nucleotide 605.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:86;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:86. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:86, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 223 to nucleotide 798;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:87 from nucleotide 430 to nucleotide 798;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk78_1 deposited under accession number ATCC 207004;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk78_1 deposited under accession number ATCC 207004;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 223 to nucleotide 798; the nucleotide sequence of SEQ ID NO:87 from nucleotide 430 to nucleotide 798; the nucleotide sequence of the full-length protein coding sequence of clone yk78_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yk78_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the

fragment comprising the amino acid sequence from amino acid 91 to amino acid 100 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(ab) the nucleotide sequence of the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(bb) the nucleotide sequence of the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 223 to nucleotide 798, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 223 to nucleotide 798, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 223 to nucleotide 798. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 430 to nucleotide 798, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 430 to nucleotide 798, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 430 to nucleotide 798.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:88;
- (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 91 to amino acid 100 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 211 to nucleotide 942;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 298 to nucleotide 942;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk251_1 deposited under accession number ATCC 207004;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk251_1 deposited under accession number ATCC 207004;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:89.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:89 from nucleotide 211 to nucleotide 942; the nucleotide sequence of SEQ ID NO:89 from nucleotide 298 to nucleotide 942; the nucleotide sequence of the full-length protein coding sequence of clone yk251_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yk251_1 deposited under accession number ATCC 207004. In other preferred embodiments, the

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polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:90.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and
 - 20 (ab) the nucleotide sequence of the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 30 (ba) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and
 - (bb) the nucleotide sequence of the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:89 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 211 to nucleotide 942, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 211 to nucleotide 942, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide
- 15 211 to nucleotide 942. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 298 to nucleotide 942, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 298 to nucleotide 942, to a nucleotide sequence corresponding to the 3' end of
- 20 said sequence of SEQ ID NO:89 from nucleotide 298 to nucleotide 942.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:90;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;

- the protein being substantially free from other mammalian proteins. Preferably such
- 30 protein comprises the amino acid sequence of SEQ ID NO:90. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:90.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 149 to nucleotide 784;
- (c) a polynucleotide comprising the nucleotide sequence of the full-
10 length protein coding sequence of clone yt14_1 deposited under accession number ATCC 207004;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
15 protein coding sequence of clone yt14_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;
- (g) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:92;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:91.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:91 from nucleotide 149 to nucleotide 784; the nucleotide sequence of the full-length

protein coding sequence of clone yt14_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yt14_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004. In further preferred
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a polynucleotide encoding
10 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 101 to amino acid 110 of SEQ ID NO:92.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:91.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
20 consisting of:

(aa) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(ab) the nucleotide sequence of the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

30 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(bb) the nucleotide sequence of the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:91 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 149 to nucleotide 784, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 149 to nucleotide 784, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 149 to nucleotide 784.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:92;

(b) a fragment of the amino acid sequence of SEQ ID NO:92, the
25 fragment comprising eight contiguous amino acids of SEQ ID NO:92; and

(c) the amino acid sequence encoded by the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:92. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 101 to amino acid 110 of SEQ ID NO:92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 89 to nucleotide 1441;
- (c) a polynucleotide comprising the nucleotide sequence of the full-
10 length protein coding sequence of clone bf157_16 deposited under accession number ATCC 207088;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
15 protein coding sequence of clone bf157_16 deposited under accession number ATCC 207088;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088;
- (g) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:94;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 89 to nucleotide 1441; the nucleotide sequence of the full-length

protein coding sequence of clone bf157_16 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone bf157_16 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088. In further preferred
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding
10 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 220 to amino acid 229 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:93, but excluding the poly(A) tail at the
3' end of SEQ ID NO:93; and

(ab) the nucleotide sequence of the cDNA insert of clone
bf157_16 deposited under accession number ATCC 207088;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

30 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(bb) the nucleotide sequence of the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 89 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 89 to nucleotide 1441, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 89 to nucleotide 1441.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:94;

25 (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and

(c) the amino acid sequence encoded by the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 220 to amino acid 229 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 219 to nucleotide 629;
- (c) a polynucleotide comprising the nucleotide sequence of the full-
10 length protein coding sequence of clone bk343_2 deposited under accession number ATCC 207088;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
15 protein coding sequence of clone bk343_2 deposited under accession number ATCC 207088;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088;
- (g) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:96;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:95.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 219 to nucleotide 629; the nucleotide sequence of the full-length

protein coding sequence of clone bk343_2 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone bk343_2 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088. In further preferred
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a polynucleotide encoding
10 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:96.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:95, but excluding the poly(A) tail at the
3' end of SEQ ID NO:95; and

(ab) the nucleotide sequence of the cDNA insert of clone
bk343_2 deposited under accession number ATCC 207088;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

30 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

(bb) the nucleotide sequence of the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 219 to nucleotide 629, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 219 to nucleotide 629, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 219 to nucleotide 629.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:96;

(b) a fragment of the amino acid sequence of SEQ ID NO:96, the
25 fragment comprising eight contiguous amino acids of SEQ ID NO:96; and

(c) the amino acid sequence encoded by the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 556 to nucleotide 951;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:97 from nucleotide 868 to nucleotide 951;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 9 to nucleotide 1295;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cd205_2 deposited under accession
15 number ATCC 207088;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cd205_2 deposited under accession number
20 ATCC 207088;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
- 25 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- 30 (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:97.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 556 to nucleotide 951; the nucleotide sequence of SEQ ID NO:97 from nucleotide 868 to nucleotide 951; the nucleotide sequence of SEQ ID NO:97 from nucleotide 9 to nucleotide 1295; the nucleotide sequence of the full-length protein coding sequence of clone cd205_2 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone cd205_2 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:98.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
 - (ab) the nucleotide sequence of the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and

10 (bb) the nucleotide sequence of the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:97. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 556 to nucleotide 951, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 556 to nucleotide 951, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 556 to nucleotide 951. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 868 to nucleotide 951, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from
30 nucleotide 868 to nucleotide 951, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 868 to nucleotide 951. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 9 to nucleotide 1295, and extending contiguously from a nucleotide sequence corresponding

to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 9 to nucleotide 1295, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 9 to nucleotide 1295.

In other embodiments, the present invention provides a composition comprising
5 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:98;
- (b) a fragment of the amino acid sequence of SEQ ID NO:98, the
fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
- 10 (c) the amino acid sequence encoded by the cDNA insert of clone
cd205_2 deposited under accession number ATCC 207088;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:98. In further preferred
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:98.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:99;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:99 from nucleotide 216 to nucleotide 443;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:99 from nucleotide 306 to nucleotide 443;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
length protein coding sequence of clone cw1292_8 deposited under accession
30 number ATCC 207088;
- (e) a polynucleotide encoding the full-length protein encoded by the
cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1292_8 deposited under accession number ATCC 207088;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:99.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:99 from nucleotide 216 to nucleotide 443; the nucleotide sequence of SEQ ID NO:99 from nucleotide 306 to nucleotide 443; the nucleotide sequence of the full-length protein coding sequence of clone cw1292_8 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone cw1292_8 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:100.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:99.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and
- (ab) the nucleotide sequence of the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 cw1292_8 deposited under accession number ATCC 207088;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:99 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 216 to nucleotide 443, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 216 to nucleotide 443, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 216 to nucleotide 443. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 306 to nucleotide 443, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 306 to nucleotide 443, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 306 to nucleotide 443.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:100;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:100. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 25 of SEQ ID NO:100, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:100.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 2136 to nucleotide 2447;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1475_2 deposited under accession number ATCC 207088;
- (d) a polynucleotide encoding the full-length protein encoded by the
5 cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1475_2 deposited under accession number ATCC 207088;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA
10 insert of clone cw1475_2 deposited under accession number ATCC 207088;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment
15 comprising eight contiguous amino acids of SEQ ID NO:102;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any
20 one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:101.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 2136 to nucleotide 2447; the nucleotide sequence of the full-length protein coding sequence of clone cw1475_2 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone cw1475_2 deposited under accession number ATCC 207088. In other preferred
30 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:102.

- 5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and
- 15 (ab) the nucleotide sequence of the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the
- 20 probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
- 25 the group consisting of:
- (ba) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and
- (bb) the nucleotide sequence of the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088;
- 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 2136 to nucleotide 2447, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 2136 to nucleotide 2447,
10 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 2136 to nucleotide 2447.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:102;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 310 to nucleotide 954;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd428_4 deposited under accession number ATCC 207088;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd428_4 deposited under accession number ATCC 207088;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment
- 15 comprising eight contiguous amino acids of SEQ ID NO:104;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:103.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 310 to nucleotide 954; the nucleotide sequence of the full-length protein coding sequence of clone dd428_4 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone dd428_4 deposited under accession number ATCC 207088. In other preferred embodiments, the
- 30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 102 to amino acid 111 of SEQ ID NO:104.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
 - 25 the group consisting of:
 - (ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
 - (bb) the nucleotide sequence of the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 310 to nucleotide 954, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 310 to nucleotide 954, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 310 to nucleotide 954.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:104;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 102 to amino acid 111 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 1698 to nucleotide 1895;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dh1073_12 deposited under accession number ATCC 207088;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dh1073_12 deposited under accession number ATCC 207088;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:105.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 1698 to nucleotide 1895; the nucleotide sequence of the full-length protein coding sequence of clone dh1073_12 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone dh1073_12 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088.
- In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:106.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and
 - (bb) the nucleotide sequence of the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 1698 to nucleotide 1895, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 1698 to nucleotide 1895,
10 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 1698 to nucleotide 1895.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:106;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 423 to nucleotide 791;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dw78_1 deposited under accession number ATCC 207088;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dw78_1 deposited under accession number ATCC 207088;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:108;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:107.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:107 from nucleotide 423 to nucleotide 791; the nucleotide sequence of the full-length protein coding sequence of clone dw78_1 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone dw78_1 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:108, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:108.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:107.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and
 - (bb) the nucleotide sequence of the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:107, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:107. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 423 to nucleotide 791, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 423 to nucleotide 791, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 423 to nucleotide 791.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:108;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:108, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:108.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 96 to nucleotide 944;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fh116_11 deposited under accession number ATCC 207088;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fh116_11 deposited under accession number ATCC 207088;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:110;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:109.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:109 from nucleotide 96 to nucleotide 944; the nucleotide sequence of the full-length protein coding sequence of clone fh116_11 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone fh116_11 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:110, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 136 to amino acid 145 of SEQ ID NO:110.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:109.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and
 - (bb) the nucleotide sequence of the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:109 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:109, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 96 to nucleotide 944, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 96 to nucleotide 944, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 96 to nucleotide 944.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:110;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:110, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 136 to amino acid 145 of SEQ ID NO:110.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 150 to nucleotide 1610;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fy356_14 deposited under accession number ATCC 207088;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fy356_14 deposited under accession number ATCC 207088;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:111.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 150 to nucleotide 1610; the nucleotide sequence of the full-length protein coding sequence of clone fy356_14 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone fy356_14 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 238 to amino acid 247 of SEQ ID NO:112.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
 - 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and
 - (bb) the nucleotide sequence of the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 150 to nucleotide 1610, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 150 to nucleotide 1610, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 150 to nucleotide 1610.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:112;
- (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
fy356_14 deposited under accession number ATCC 207088;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 238 to amino acid 247 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 49 to nucleotide 669;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 112 to nucleotide 669;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone iw66_1 deposited under accession number ATCC 207088;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone iw66_1 deposited under accession number ATCC 207088;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:114;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:113.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:113 from nucleotide 49 to nucleotide 669; the nucleotide sequence of SEQ ID NO:113 from nucleotide 112 to nucleotide 669; the nucleotide sequence of the full-length protein coding sequence of clone iw66_1 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone iw66_1 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088. In further preferred embodiments, the

present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a polynucleotide encoding a protein comprising a
5 fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 98 to amino acid 107 of SEQ ID NO:114.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:113.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
15 consisting of:

(aa) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(ab) the nucleotide sequence of the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(bb) the nucleotide sequence of the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide
10 669, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 49 to nucleotide 669, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 49 to nucleotide 669. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:113 from nucleotide 112 to nucleotide 669, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 112 to nucleotide 669, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 112 to nucleotide 669.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:114;
- (b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:114. In further preferred embodiments, the present invention provides a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 98 to amino acid 107 of SEQ ID NO:114.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 165 to nucleotide 416;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone kh13_4 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone kh13_4 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:116;
- (h) a polynucleotide encoding a protein comprising a fragment of the
20 amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein
25 of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
30 25% of the length of SEQ ID NO:115.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:115 from nucleotide 165 to nucleotide 416; the nucleotide sequence of the full-length protein coding sequence of clone kh13_4 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone kh13_4

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:116.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:115.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (aa) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and
 - (ab) the nucleotide sequence of the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and

- (bb) the nucleotide sequence of the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:115 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 165 to nucleotide 416, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 165 to nucleotide 416, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 165 to nucleotide 416.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:116;
- (b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and
- (c) the amino acid sequence encoded by the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 204 to nucleotide 602;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ko258_4 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ko258_4 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:118;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:117.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:117 from nucleotide 204 to nucleotide 602; the nucleotide sequence of the full-length protein coding sequence of clone ko258_4 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone ko258_4

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein
5 comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino
10 acid 61 to amino acid 70 of SEQ ID NO:118.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:117.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 20 (aa) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and
- (ab) the nucleotide sequence of the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

- (bb) the nucleotide sequence of the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:117 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117 from nucleotide 204 to nucleotide 602, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 204 to nucleotide 602, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide 204 to nucleotide 602.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:118;
- (b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:118. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:118.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119 from nucleotide 434 to nucleotide 739;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone kv10_8 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone kv10_8 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:120;
- (h) a polynucleotide encoding a protein comprising a fragment of the
20 amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:120;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein
25 of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
30 25% of the length of SEQ ID NO:119.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:119 from nucleotide 434 to nucleotide 739; the nucleotide sequence of the full-length protein coding sequence of clone kv10_8 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone kv10_8

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:120.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:119.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (aa) SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119; and
 - (ab) the nucleotide sequence of the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119; and

- (bb) the nucleotide sequence of the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

10 ID NO:119 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119 from nucleotide 434 to nucleotide 739, and extending contiguously from a nucleotide sequence corresponding to the 5' end

15 of said sequence of SEQ ID NO:119 from nucleotide 434 to nucleotide 739, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:119 from nucleotide 434 to nucleotide 739.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

20 consisting of:

- (a) the amino acid sequence of SEQ ID NO:120;
- (b) a fragment of the amino acid sequence of SEQ ID NO:120, the fragment comprising eight contiguous amino acids of SEQ ID NO:120; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
- 25 kv10_8 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:120. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment preferably

30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:120.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121 from nucleotide 149 to nucleotide 310;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone LL89_3 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone LL89_3 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:122;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:122;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:121.
- 30

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:121 from nucleotide 149 to nucleotide 310; the nucleotide sequence of the full-length protein coding sequence of clone LL89_3 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone LL89_3

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:122, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:122.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:121.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (aa) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and
 - (ab) the nucleotide sequence of the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and

- (bb) the nucleotide sequence of the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:121 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121 from nucleotide 149 to nucleotide 310, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:121 from nucleotide 149 to nucleotide 310, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:121 from nucleotide 149 to nucleotide 310.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:122;
- (b) a fragment of the amino acid sequence of SEQ ID NO:122, the fragment comprising eight contiguous amino acids of SEQ ID NO:122; and
- (c) the amino acid sequence encoded by the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089;

25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:122. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:122, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:122.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123 from nucleotide 22 to nucleotide 288;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mc300_1 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mc300_1 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:124;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:124;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:123.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:123 from nucleotide 22 to nucleotide 288; the nucleotide sequence of the full-length protein coding sequence of clone mc300_1 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone mc300_1

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:124.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:123.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (aa) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and
 - (ab) the nucleotide sequence of the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and

- (bb) the nucleotide sequence of the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
10 ID NO:123 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123 from nucleotide 22 to nucleotide 288, and extending contiguously from a nucleotide sequence corresponding to the 5' end
15 of said sequence of SEQ ID NO:123 from nucleotide 22 to nucleotide 288, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide 22 to nucleotide 288.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
20 consisting of:

- (a) the amino acid sequence of SEQ ID NO:124;
- (b) a fragment of the amino acid sequence of SEQ ID NO:124, the fragment comprising eight contiguous amino acids of SEQ ID NO:124; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
25 mc300_1 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:124. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:124.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 200 to nucleotide 2449;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml227_1 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml227_1 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:126;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:126;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:125.
- 30

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:125 from nucleotide 200 to nucleotide 2449; the nucleotide sequence of the full-length protein coding sequence of clone ml227_1 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone ml227_1

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 370 to amino acid 379 of SEQ ID NO:126.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:125.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (aa) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and

(bb) the nucleotide sequence of the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
10 ID NO:125 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 200 to nucleotide 2449, and extending contiguously from a nucleotide sequence corresponding to the 5' end
15 of said sequence of SEQ ID NO:125 from nucleotide 200 to nucleotide 2449, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 200 to nucleotide 2449.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
20 consisting of:

(a) the amino acid sequence of SEQ ID NO:126;

(b) a fragment of the amino acid sequence of SEQ ID NO:126, the fragment comprising eight contiguous amino acids of SEQ ID NO:126; and

(c) the amino acid sequence encoded by the cDNA insert of clone
25 ml227_1 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:126. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 370 to amino acid 379 of SEQ ID NO:126.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 82 to nucleotide 1980;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mm367_6 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mm367_6 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:128;
- (h) a polynucleotide encoding a protein comprising a fragment of the
20 amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:128;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein
25 of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
30 25% of the length of SEQ ID NO:127.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:127 from nucleotide 82 to nucleotide 1980; the nucleotide sequence of the full-length protein coding sequence of clone mm367_6 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone mm367_6

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 311 to amino acid 320 of SEQ ID NO:128.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:127.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (aa) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and
 - (ab) the nucleotide sequence of the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
-) and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 30 (ba) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and

- (bb) the nucleotide sequence of the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
10 ID NO:127 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 82 to nucleotide 1980, and extending contiguously from a nucleotide sequence corresponding to the 5' end
15 of said sequence of SEQ ID NO:127 from nucleotide 82 to nucleotide 1980, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 82 to nucleotide 1980.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
20 consisting of:

- (a) the amino acid sequence of SEQ ID NO:128;
- (b) a fragment of the amino acid sequence of SEQ ID NO:128, the fragment comprising eight contiguous amino acids of SEQ ID NO:128; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
25 mm367_6 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:128. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 311 to amino acid 320 of SEQ ID NO:128.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 125 to nucleotide 856;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mt124_3 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mt124_3 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:130;
- (h) a polynucleotide encoding a protein comprising a fragment of the
20 amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:130;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein
25 of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
30 25% of the length of SEQ ID NO:129.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:129 from nucleotide 125 to nucleotide 856; the nucleotide sequence of the full-length protein coding sequence of clone mt124_3 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone mt124_3

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:130, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:130.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:129.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (aa) SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129; and
 - (ab) the nucleotide sequence of the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129; and

- (bb) the nucleotide sequence of the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:129 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 125 to nucleotide 856, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 125 to nucleotide 856, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 125 to nucleotide 856.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:130;
- (b) a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130; and
- (c) the amino acid sequence encoded by the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:130. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:130, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:130.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 856 to nucleotide 2940;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 901 to nucleotide 2940;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nf56_3 deposited under accession number ATCC 207089;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nf56_3 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:132;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:132;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:131.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:131 from nucleotide 856 to nucleotide 2940; the nucleotide sequence of SEQ ID

NO:131 from nucleotide 901 to nucleotide 2940; the nucleotide sequence of the full-length protein coding sequence of clone nf56_3 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone nf56_3 deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:132, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 342 to amino acid 351 of SEQ ID NO:132.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:131.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and
 - (ab) the nucleotide sequence of the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and

(bb) the nucleotide sequence of the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:131 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 856 to nucleotide 2940, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 856 to nucleotide 2940, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 856 to nucleotide 2940. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 901 to nucleotide 2940, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 901 to nucleotide 2940, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 901 to nucleotide 2940.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:132;

(b) a fragment of the amino acid sequence of SEQ ID NO:132, the
30 fragment comprising eight contiguous amino acids of SEQ ID NO:132; and

(c) the amino acid sequence encoded by the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:132. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:132, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 342 to amino acid 351 of SEQ ID NO:132.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133 from nucleotide 122 to nucleotide 448;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133 from nucleotide 167 to nucleotide 448;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qy442_2 deposited under accession number ATCC 207089;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qy442_2 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:134;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:134;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:133.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:133 from nucleotide 122 to nucleotide 448; the nucleotide sequence of SEQ ID NO:133 from nucleotide 167 to nucleotide 448; the nucleotide sequence of the full-length protein coding sequence of clone qy442_2 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone qy442_2 deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:134, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 49 to amino acid 58 of SEQ ID NO:134.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:133.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:133, but excluding the poly(A) tail at the 3' end of SEQ ID NO:133; and

(ab) the nucleotide sequence of the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:133, but excluding the poly(A) tail at the 3' end of SEQ ID NO:133; and

10 (bb) the nucleotide sequence of the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:133 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:133, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:133. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133 from nucleotide 122 to nucleotide 448, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:133 from nucleotide 122 to nucleotide 448, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:133 from nucleotide 122 to nucleotide 448. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133 from nucleotide 167 to nucleotide 448, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:133 from
30 nucleotide 167 to nucleotide 448, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:133 from nucleotide 167 to nucleotide 448.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:134;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:134, the fragment comprising eight contiguous amino acids of SEQ ID NO:134; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:134. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably
- 10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:134, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 49 to amino acid 58 of SEQ ID NO:134.

In one embodiment, the present invention provides a composition comprising an

15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:135;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:135 from nucleotide 28 to nucleotide 777;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:135 from nucleotide 73 to nucleotide 777;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rj214_14 deposited under accession number ATCC 207089;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rj214_14 deposited under accession number ATCC 207089;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:136;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:136;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:135.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:135 from nucleotide 28 to nucleotide 777; the nucleotide sequence of SEQ ID NO:135 from nucleotide 73 to nucleotide 777; the nucleotide sequence of the full-length protein coding sequence of clone rj214_14 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone rj214_14 deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:136, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID NO:136.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:135.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135; and

(ab) the nucleotide sequence of the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135; and

(bb) the nucleotide sequence of the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:135, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:135 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:135 from nucleotide 28 to nucleotide 777, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:135 from nucleotide 28 to nucleotide 777, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:135 from nucleotide

28 to nucleotide 777. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:135 from nucleotide 73 to nucleotide 777, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:135 from
5 nucleotide 73 to nucleotide 777, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:135 from nucleotide 73 to nucleotide 777.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:136;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:136, the fragment comprising eight contiguous amino acids of SEQ ID NO:136; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:136. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:136, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID NO:136.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:137;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:137 from nucleotide 179 to nucleotide 745;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:137 from nucleotide 233 to nucleotide 745;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rk80_3 deposited under accession number ATCC 207089;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rk80_3 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:138;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:138;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:137.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:137 from nucleotide 179 to nucleotide 745; the nucleotide sequence of SEQ ID NO:137 from nucleotide 233 to nucleotide 745; the nucleotide sequence of the full-length protein coding sequence of clone rk80_3 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone rk80_3 deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:138, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the

fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:138.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:137.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137; and

(ab) the nucleotide sequence of the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137; and

(bb) the nucleotide sequence of the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:137, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:137 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:137 from nucleotide 179 to nucleotide 745, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:137 from nucleotide 179 to nucleotide 745, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:137 from nucleotide 179 to nucleotide 745. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:137 from nucleotide 233 to nucleotide 745, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:137 from nucleotide 233 to nucleotide 745, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:137 from nucleotide 233 to nucleotide 745.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:138;
- (b) a fragment of the amino acid sequence of SEQ ID NO:138, the fragment comprising eight contiguous amino acids of SEQ ID NO:138; and
- (c) the amino acid sequence encoded by the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:138. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:138, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:138.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:139;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:139 from nucleotide 1017 to nucleotide 1274;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone au36_42 deposited under accession number ATCC 207187;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone au36_42 deposited under accession number ATCC 207187;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone au36_42 deposited under accession number ATCC 207187;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone au36_42 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:140;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:140;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:139.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:139 from nucleotide 1017 to nucleotide 1274; the nucleotide sequence of the full-length protein coding sequence of clone au36_42 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone au36_42 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone au36_42 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding

- a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:140, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140
- 5 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:140.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:139.

- Further embodiments of the invention provide isolated polynucleotides produced
- 10 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 15 (aa) SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139; and
 - (ab) the nucleotide sequence of the cDNA insert of clone au36_42 deposited under accession number ATCC 207187;
 - (ii) hybridizing said probe(s) to human genomic DNA in
 - 20 conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - 25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139; and
 - 30 (bb) the nucleotide sequence of the cDNA insert of clone au36_42 deposited under accession number ATCC 207187;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and

- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:139, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:139 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:139 from nucleotide 1017 to nucleotide 1274, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:139 from nucleotide 1017 to nucleotide 1274, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:139 from nucleotide 1017 to nucleotide 1274.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:140;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:140, the fragment comprising eight contiguous amino acids of SEQ ID NO:140; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone au36_42 deposited under accession number ATCC 207187;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:140. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:140, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:140.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:141;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:141 from nucleotide 580 to nucleotide 774;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bo549_13 deposited under accession number ATCC 207187;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bo549_13 deposited under accession number ATCC 207187;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:142;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:142;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:141.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:141 from nucleotide 580 to nucleotide 774; the nucleotide sequence of the full-length protein coding sequence of clone bo549_13 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone bo549_13 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:142, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment comprising the amino acid sequence from amino acid 27 to amino acid 36 of SEQ ID NO:142.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:141.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:141, but excluding the poly(A) tail at the 3' end of SEQ ID NO:141; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:141, but excluding the poly(A) tail at the 3' end of SEQ ID NO:141; and
 - (bb) the nucleotide sequence of the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:141, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:141 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:141, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:141. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:141 from nucleotide 580 to nucleotide 774, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:141 from nucleotide 580 to nucleotide 774, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:141 from nucleotide 580 to nucleotide 774.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:142;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:142, the fragment comprising eight contiguous amino acids of SEQ ID NO:142; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:142. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:142, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment comprising the amino acid sequence from amino acid 27 to amino acid 36 of SEQ ID NO:142.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:143;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:143 from nucleotide 172 to nucleotide 969;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:143 from nucleotide 385 to nucleotide 969;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone da529_3 deposited under accession number ATCC 207187;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone da529_3 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:144;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:144;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:143.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:143 from nucleotide 172 to nucleotide 969; the nucleotide sequence of SEQ ID NO:143 from nucleotide 385 to nucleotide 969; the nucleotide sequence of the full-length protein coding sequence of clone da529_3 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone da529_3 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone da529_3 deposited under accession number ATCC 207187. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:144, or a polynucleotide
5 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment comprising the amino acid sequence from amino acid 128 to amino acid 137 of SEQ ID NO:144.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:143.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
15 consisting of:

(aa) SEQ ID NO:143, but excluding the poly(A) tail at the 3' end of SEQ ID NO:143; and

(ab) the nucleotide sequence of the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:143, but excluding the poly(A) tail at the 3' end of SEQ ID NO:143; and

(bb) the nucleotide sequence of the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:143, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:143 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:143, but excluding the poly(A) tail at the 3' end of SEQ ID NO:143. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:143 from nucleotide 172 to nucleotide
10 969, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:143 from nucleotide 172 to nucleotide 969, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:143 from nucleotide 172 to nucleotide 969. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:143 from nucleotide 385 to nucleotide 969, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:143 from nucleotide 385 to nucleotide 969, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:143 from nucleotide 385 to nucleotide 969.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:144;
- (b) a fragment of the amino acid sequence of SEQ ID NO:144, the fragment comprising eight contiguous amino acids of SEQ ID NO:144; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:144. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:144, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment comprising the amino acid sequence from amino acid 128 to amino acid 137 of SEQ ID NO:144.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:145;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:145 from nucleotide 329 to nucleotide 667;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:145 from nucleotide 368 to nucleotide 667;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dm365_3 deposited under accession number ATCC 207187;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dm365_3 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:146;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:146;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:145.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:145 from nucleotide 329 to nucleotide 667; the nucleotide sequence of SEQ ID NO:145

from nucleotide 368 to nucleotide 667; the nucleotide sequence of the full-length protein coding sequence of clone dm365_3 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone dm365_3 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:146, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:146.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:145.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:145, but excluding the poly(A) tail at the 3' end of SEQ ID NO:145; and
 - (ab) the nucleotide sequence of the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:145, but excluding the poly(A) tail at the 3' end of SEQ ID NO:145; and

(bb) the nucleotide sequence of the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:145, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:145 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:145, but excluding the poly(A) tail at the 3' end of SEQ ID NO:145. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:145 from nucleotide 329 to nucleotide 667, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:145 from nucleotide 329 to nucleotide 667, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:145 from nucleotide 329 to nucleotide 667. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:145 from nucleotide 368 to nucleotide 667, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:145 from nucleotide 368 to nucleotide 667, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:145 from nucleotide 368 to nucleotide 667.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:146;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:146, the fragment comprising eight contiguous amino acids of SEQ ID NO:146; and

(c) the amino acid sequence encoded by the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:146. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:146, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:146.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:147;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:147 from nucleotide 103 to nucleotide 1368;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fa171_1 deposited under accession number ATCC 207187;
- 15 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fa171_1 deposited under accession number ATCC 207187;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:148;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:148;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 30 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:147.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:147 from nucleotide 103 to nucleotide 1368; the nucleotide sequence of the full-length protein coding sequence of clone fa171_1 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone fa171_1 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:148, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising the amino acid sequence from amino acid 206 to amino acid 215 of SEQ ID NO:148.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:147.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147; and

(ab) the nucleotide sequence of the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147; and

(bb) the nucleotide sequence of the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:147, and
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:147 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:147 from nucleotide 103 to nucleotide
20 1368, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:147 from nucleotide 103 to nucleotide 1368, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:147 from nucleotide 103 to nucleotide 1368.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:148;

(b) a fragment of the amino acid sequence of SEQ ID NO:148, the fragment comprising eight contiguous amino acids of SEQ ID NO:148; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:148. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:148 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:148, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising the amino acid sequence
5 from amino acid 206 to amino acid 215 of SEQ ID NO:148.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:149;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:149 from nucleotide 190 to nucleotide 1407;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:149 from nucleotide 463 to nucleotide 1407;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone lp572_2 deposited under accession
15 number ATCC 207187;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
20 protein coding sequence of clone lp572_2 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187;
- (h) a polynucleotide encoding a protein comprising the amino acid
25 sequence of SEQ ID NO:150;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:150;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:149.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
5 NO:149 from nucleotide 190 to nucleotide 1407; the nucleotide sequence of SEQ ID
NO:149 from nucleotide 463 to nucleotide 1407; the nucleotide sequence of the full-length
protein coding sequence of clone lp572_2 deposited under accession number ATCC
207187; or the nucleotide sequence of a mature protein coding sequence of clone lp572_2
deposited under accession number ATCC 207187. In other preferred embodiments, the
10 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert
of clone lp572_2 deposited under accession number ATCC 207187. In further preferred
embodiments, the present invention provides a polynucleotide encoding a protein
comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological
activity, the fragment preferably comprising eight (more preferably twenty, most
15 preferably thirty) contiguous amino acids of SEQ ID NO:150, or a polynucleotide
encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150
having biological activity, the fragment comprising the amino acid sequence from amino
acid 198 to amino acid 207 of SEQ ID NO:150.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
20 ID NO:149.

Further embodiments of the invention provide isolated polynucleotides produced
according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
consisting of:
 - (aa) SEQ ID NO:149, but excluding the poly(A) tail at the
3' end of SEQ ID NO:149; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
30 lp572_2 deposited under accession number ATCC 207187;
 - (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the
probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:149, but excluding the poly(A) tail at the 3' end of SEQ ID NO:149; and

(bb) the nucleotide sequence of the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:149 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:149, but excluding the poly(A) tail at the 3' end of SEQ ID NO:149. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149 from nucleotide 190 to nucleotide 1407, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:149 from nucleotide 190 to nucleotide 1407, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:149 from nucleotide 190 to nucleotide 1407. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149 from nucleotide 463 to nucleotide 1407, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:149 from nucleotide 463 to nucleotide 1407, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:149 from nucleotide 463 to nucleotide 1407.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:150;

(b) a fragment of the amino acid sequence of SEQ ID NO:150, the fragment comprising eight contiguous amino acids of SEQ ID NO:150; and

(c) the amino acid sequence encoded by the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187;

- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:150. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:150, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment comprising the amino acid sequence from amino acid 198 to amino acid 207 of SEQ ID NO:150.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:151;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:151 from nucleotide 301 to nucleotide 1035;

- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:151 from nucleotide 916 to nucleotide 1035;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe246_1 deposited under accession number ATCC 207187;

- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe246_1 deposited under accession number ATCC 207187;

- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:152;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:152;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:151.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:151 from nucleotide 301 to nucleotide 1035; the nucleotide sequence of SEQ ID NO:151 from nucleotide 916 to nucleotide 1035; the nucleotide sequence of the full-length protein coding sequence of clone pe246_1 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone pe246_1 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:152, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:152.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:151.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151; and

(ab) the nucleotide sequence of the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151; and

(bb) the nucleotide sequence of the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:151, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:151 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:151 from nucleotide 301 to nucleotide 1035, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:151 from nucleotide 301 to nucleotide 1035, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:151 from nucleotide

301 to nucleotide 1035. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:151 from nucleotide 916 to nucleotide 1035, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:151 from
5 nucleotide 916 to nucleotide 1035, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:151 from nucleotide 916 to nucleotide 1035.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:152;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:152, the fragment comprising eight contiguous amino acids of SEQ ID NO:152; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:152. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:152, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:152.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:153;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:153 from nucleotide 94 to nucleotide 1281;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qf122_3 deposited under accession
30 number ATCC 207187;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qf122_3 deposited under accession number ATCC 207187;
- 5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:154;
- 10 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:154;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 15 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:153.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:153 from nucleotide 94 to nucleotide 1281; the nucleotide sequence of the full-length protein coding sequence of clone qf122_3 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone qf122_3 deposited under accession number ATCC 207187. In other preferred embodiments, the
- 25 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
- 30 preferably thirty) contiguous amino acids of SEQ ID NO:154, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising the amino acid sequence from amino acid 193 to amino acid 202 of SEQ ID NO:154.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:153.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:153; and
- 10 (ab) the nucleotide sequence of the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- 15 and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 20 (ba) SEQ ID NO:153; and
- (bb) the nucleotide sequence of the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 25 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:153, and

30 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:153 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:153. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:153 from nucleotide 94 to nucleotide 1281, and extending contiguously from a nucleotide sequence

corresponding to the 5' end of said sequence of SEQ ID NO:153 from nucleotide 94 to nucleotide 1281, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:153 from nucleotide 94 to nucleotide 1281.

In other embodiments, the present invention provides a composition comprising
5 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:154;
- (b) a fragment of the amino acid sequence of SEQ ID NO:154, the
fragment comprising eight contiguous amino acids of SEQ ID NO:154; and
- 10 (c) the amino acid sequence encoded by the cDNA insert of clone
qf122_3 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:154. In further preferred
15 amino acid sequence of SEQ ID NO:154 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:154, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising the amino acid sequence from amino acid 193 to amino acid 202 of SEQ ID NO:154.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:155;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:155 from nucleotide 110 to nucleotide 742;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:155 from nucleotide 170 to nucleotide 742;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
length protein coding sequence of clone qv538_1 deposited under accession
30 number ATCC 207187;
- (e) a polynucleotide encoding the full-length protein encoded by the
cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qv538_1 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:156;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:156;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:155.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:155 from nucleotide 110 to nucleotide 742; the nucleotide sequence of SEQ ID NO:155 from nucleotide 170 to nucleotide 742; the nucleotide sequence of the full-length protein coding sequence of clone qv538_1 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone qv538_1 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:156, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO:156.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:155.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:155, but excluding the poly(A) tail at the 3' end of SEQ ID NO:155; and
- (ab) the nucleotide sequence of the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:155, but excluding the poly(A) tail at the 3' end of SEQ ID NO:155; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 qv538_1 deposited under accession number ATCC 207187;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:155 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:155, but excluding the poly(A) tail at the 3' end of SEQ ID NO:155. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155 from nucleotide 110 to nucleotide 742, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:155 from nucleotide 110 to nucleotide 742, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:155 from nucleotide 110 to nucleotide 742. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155 from nucleotide 170 to nucleotide 742, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:155 from nucleotide 170 to nucleotide 742, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:155 from nucleotide 170 to nucleotide 742.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:156;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:156, the fragment comprising eight contiguous amino acids of SEQ ID NO:156; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:156. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:156, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO:156.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:157;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:157 from nucleotide 41 to nucleotide 757;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ys20_1 deposited under accession number ATCC 207187;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ys20_1 deposited under accession number ATCC 207187;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:158;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:158;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:157.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:157 from nucleotide 41 to nucleotide 757; the nucleotide sequence of the full-length protein coding sequence of clone ys20_1 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone ys20_1 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:158, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:158.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:157.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and
 - (bb) the nucleotide sequence of the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:157, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:157 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:157, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:157. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:157 from nucleotide 41 to nucleotide 757, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:157 from nucleotide 41 to nucleotide 757, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:157 from nucleotide 41 to nucleotide 757.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:158;
- (b) a fragment of the amino acid sequence of SEQ ID NO:158, the fragment comprising eight contiguous amino acids of SEQ ID NO:158; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
ys20_1 deposited under accession number ATCC 207187;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:158. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:158, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:158.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:159;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:159 from nucleotide 28 to nucleotide 2253;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:159 from nucleotide 568 to nucleotide 2253;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone as180_1 deposited under accession number ATCC XXXXXX;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone as180_1 deposited under accession number ATCC XXXXXX;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:160;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:160;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:159.
- 25

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:159 from nucleotide 28 to nucleotide 2253; the nucleotide sequence of SEQ ID NO:159 from nucleotide 568 to nucleotide 2253; the nucleotide sequence of the full-length protein coding sequence of clone as180_1 deposited under accession number ATCC XXXXXX; or the nucleotide sequence of a mature protein coding sequence of clone as180_1 deposited under accession number ATCC XXXXXX. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX. In further

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preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:160, or a polynucleotide
5 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment comprising the amino acid sequence from amino acid 366 to amino acid 375 of SEQ ID NO:160.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:159.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
15 consisting of:

- (aa) SEQ ID NO:159; and

- (ab) the nucleotide sequence of the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;

- (ii) hybridizing said probe(s) to human genomic DNA in
20 conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that
25 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:159; and

- (bb) the nucleotide sequence of the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;

- (ii) hybridizing said primer(s) to human genomic DNA in
30 conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and

- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:159, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:159 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:159. Also

5 preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:159 from nucleotide 28 to nucleotide 2253, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:159 from nucleotide 28 to nucleotide 2253, to a nucleotide sequence corresponding to the 3' end of said sequence of

10 SEQ ID NO:159 from nucleotide 28 to nucleotide 2253. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:159 from nucleotide 568 to nucleotide 2253, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:159 from nucleotide 568 to nucleotide 2253, to a nucleotide

15 sequence corresponding to the 3' end of said sequence of SEQ ID NO:159 from nucleotide 568 to nucleotide 2253.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:160;
- (b) a fragment of the amino acid sequence of SEQ ID NO:160, the fragment comprising eight contiguous amino acids of SEQ ID NO:160; and
- (c) the amino acid sequence encoded by the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:160. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 30 of SEQ ID NO:160, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment comprising the amino acid sequence from amino acid 366 to amino acid 375 of SEQ ID NO:160.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial,

yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

5 Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present
10 invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical
15 condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

BRIEF DESCRIPTION OF THE DRAWINGS

20 Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

Figure 2 is a schematic representation of the pCMVSPORT2 vector used for deposit of clone qs14_3 disclosed herein.

DETAILED DESCRIPTION

ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone
30 in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have

determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

10 Clone "co62_12"

A polynucleotide of the present invention has been identified as clone "co62_12". co62_12 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. co62_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "co62_12 protein").

The nucleotide sequence of co62_12 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the co62_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 1 to 11 of SEQ ID NO:2 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 12. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the co62_12 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone co62_12 should be approximately 2200 bp.

The nucleotide sequence disclosed herein for co62_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. co62_12 demonstrated at least some similarity with sequences identified as AA019597 (ze60f10.s1 Soares retina N2b4HR Homo sapiens cDNA), AA021678 (mh82c02.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus), AA057573 (zf62d10.s1 Soares retina N2b4HR Homo sapiens cDNA clone 381523 3' similar to WP

T12G3.4 CE06440 STRICTOSIDINE SYNTHASE LIKE, mRNA sequence), AA130982, AA287697 (zs53g02.r1 Soares NbHTGBC Homo sapiens cDNA clone 701234 5'), AI042188 (oy37d10.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668019 3' similar to WP:F57C2.5 CE16156, mRNA sequence), R63905 (yi19b03.s1
5 Homo sapiens cDNA clone 139661 3'), T03538 (IB43 Infant brain, Bento Soares Homo sapiens cDNA clone IB43 3'end), T20257 (Human gene signature HUMGS01405), and T23663 (seq294 Homo sapiens cDNA clone b4HB3MA-Cot109+103-Bio-24 3'). The predicted amino acid sequence disclosed herein for co62_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.
10 The predicted co62_12 protein demonstrated at least some similarity to sequences identified as R88502 (Protein sequence for mediating male fertility in plants) and Z83110 (F57C2.5 [Caenorhabditis elegans]). Based upon sequence similarity, co62_12 proteins and each similar protein or peptide may share at least some activity.

15 Clone "lo311_8"

A polynucleotide of the present invention has been identified as clone "lo311_8". lo311_8 was isolated from a human adult thyroid cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
20 analysis of the amino acid sequence of the encoded protein. lo311_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "lo311_8 protein").

The nucleotide sequence of lo311_8 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper
25 reading frame and the predicted amino acid sequence of the lo311_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino acids 17 to 29 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain
30 should the predicted leader/signal sequence not be separated from the remainder of the lo311_8 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone lo311_8 should be approximately 3850 bp.

The nucleotide sequence disclosed herein for lo311_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. lo311_8 demonstrated at least some similarity with sequences identified as AA046836 (zf14b10.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 376891 5' similar to WP:ZK686.3 CE00457), AA297716 (EST113273 Infant adrenal gland, subtracted (total cDNA) I Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK686_3), AF008554 (Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds), T68050 (yc39h10.r1 Homo sapiens cDNA clone 83107 5' similar to SP ZK686.3 CE00457), and U42349 (Human N33 mRNA, complete cds). The predicted amino acid sequence disclosed herein for lo311_8 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted lo311_8 protein demonstrated at least some similarity to sequences identified as AF008554 (implantation-associated protein [Rattus norvegicus]), R85333 (Human prostate/colon tumour suppressor protein form 1) and U42349 (39 kDa encoded by N33 [Homo sapiens]). Based upon sequence similarity, lo311_8 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the lo311_8 protein sequence, centered around amino acids 10, 190, 220, 275, and 310 of SEQ ID NO:4, respectively.

20

Clone "ns197_1"

A polynucleotide of the present invention has been identified as clone "ns197_1". ns197_1 was isolated from a human adult retina (retinoblastoma WERI-Rb1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ns197_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ns197_1 protein").

The nucleotide sequence of ns197_1 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ns197_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ns197_1 should be approximately 3650 bp.

The nucleotide sequence disclosed herein for ns197_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ns197_1 demonstrated at least some similarity with sequences identified as AA495135 (fa03c11.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 3K8 5' similar to WP:ZC518.3 CE06603 ALCOHOL DEHYDROGENASE TRANSCRIPTION EFFECTOR LIKE; mRNA sequence). The predicted amino acid sequence disclosed herein for ns197_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ns197_1 protein demonstrated at least some similarity to the sequence identified as Z68753 (ZC518.3 [Caenorhabditis elegans]). Based upon sequence similarity, ns197_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the ns197_1 protein sequence centered around amino acid 135 of SEQ ID NO:6. The nucleotide sequence of ns197_1 indicates that it may contain one or more repeat sequences, including primate simple repeat GCC, Alu, and other repetitive elements.

Clone "pj193_5"

A polynucleotide of the present invention has been identified as clone "pj193_5". pj193_5 was isolated from a human fetal carcinoma (NTD2 cells, treated with retinoic acid for 23 days) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pj193_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pj193_5 protein").

The nucleotide sequence of pj193_5 as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pj193_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8. Amino acids 9 to 21 of SEQ ID NO:8 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pj193_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pj193_5 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for pj193_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pj193_5 demonstrated at least some similarity with sequences identified as AA296889 (EST112653 Cerebellum II Homo sapiens cDNA 5' end), AA296961 (EST112514 Adrenal gland tumor Homo sapiens cDNA 5' end), AA661635 (nv02g06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219066), and U80744 (Homo sapiens CTG4a mRNA, complete cds). The predicted amino acid sequence disclosed herein for pj193_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pj193_5 protein demonstrated at least some similarity to the sequence identified as U80744 (CTG4a [Homo sapiens]). Based upon sequence similarity, pj193_5 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of pj193_5 indicates that it may contain CAG nucleotide repeats; these repeats may create a "hotspot" for certain types of mutations. "Twelve diseases, most with neuropsychiatric features, arise from trinucleotide repeat expansion mutations. Expansion mutations may also cause a number of other disorders, including several additional forms of spinocerebellar ataxia, bipolar affective disorder, schizophrenia, and autism." (Margolis *et al.*, 1997, *Human Genetics* 100(1): 114-122, which is incorporated by reference herein.) It is possible that the gene corresponding to pj193_5 undergoes a similar etiology.

pj193_5 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 31 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "pj317_2"

A polynucleotide of the present invention has been identified as clone "pj317_2". pj317_2 was isolated from a human fetal carcinoma (NTD2 cells, treated with retinoic acid for 23 days) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pj317_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pj317_2 protein").

The nucleotide sequence of pj317_2 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pj317_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10.

- 5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pj317_2 should be approximately 2300 bp.

 The nucleotide sequence disclosed herein for pj317_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pj317_2 demonstrated at least some similarity with sequences
10 identified as AA305508 (EST176494 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence), AA471379 (PMY1151 KG1a Lambda Zap Express cDNA Library Homo sapiens cDNA 5', mRNA sequence), and AA906311 (ok03f08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1506759 3', mRNA sequence). The predicted amino acid sequence disclosed herein for pj317_2 was searched against the
15 GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pj317_2 protein demonstrated at least some similarity to the sequences identified as U37763 (Per9p [Pichia angusta]) and U56965 (Caenorhabditis elegans cosmid C15H9). Per9p is a peroxisomal membrane protein, and the predicted pj317_2 protein demonstrated at least some similarity to peroxisomal proteins from other species as well.
20 Based upon sequence similarity, pj317_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pj317_2 protein sequence centered around amino acid 25 of SEQ ID NO:10. The nucleotide sequence of pj317_2 indicates that it may contain a simple AT and MER repeat region.

25

Clone "pt332_1"

 A polynucleotide of the present invention has been identified as clone "pt332_1". pt332_1 was isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S.
30 Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pt332_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pt332_1 protein").

The nucleotide sequence of pt332_1 as presently determined is reported in SEQ ID NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pt332_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12. Amino acids 287 to 299 of SEQ ID NO:12 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 300. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pt332_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pt332_1 should be approximately 3450 bp.

The nucleotide sequence disclosed herein for pt332_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pt332_1 demonstrated at least some similarity with sequences identified as AA167221 (zp13c09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 609328 3'), AA437109 (zv53c07.s1 Soares testis NHT Homo sapiens cDNA clone 757356 3'), H14107 (ym62a06.r1 Homo sapiens cDNA clone 163474 5'), and U41264 (C. elegans cDNA). Based upon sequence similarity, pt332_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pt332_1 protein sequence centered around amino acid 270 of SEQ ID NO:12.

pt332_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 100 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

25

Clone "qc297_15"

A polynucleotide of the present invention has been identified as clone "qc297_15". qc297_15 was isolated from a human adult neural (neuroepithelioma HTB-10 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qc297_15 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qc297_15 protein").

30

The nucleotide sequence of qc297_15 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qc297_15 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14.

- 5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qc297_15 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for qc297_15 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qc297_15 demonstrated at least some similarity with sequences
10 identified as AA625537 (af72g07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 1047612 5') and T24537 (EST112 Homo sapiens cDNA clone 4H3). Based upon sequence similarity, qc297_15 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the qc297_15 protein sequence, around amino acid 20 of SEQ ID NO:14. The
15 nucleotide/amino acid sequence of qc297_15 indicates that it may contain an Alu/SVA/MER repeat region.

qc297_15 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 7 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

20

Clone "qg596_12"

A polynucleotide of the present invention has been identified as clone "qg596_12". qg596_12 was isolated from a human adult neural (neuroepithelioma HTB-10 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins
25 (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qg596_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qg596_12 protein").

The nucleotide sequence of qg596_12 as presently determined is reported in SEQ
30 ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qg596_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qg596_12 should be approximately 2750 bp.

The nucleotide sequence disclosed herein for qg596_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qg596_12 demonstrated at least some similarity with sequences identified as AA332939 (EST37132 Embryo, 8 week I Homo sapiens cDNA 5' end),
5 AA334678 (EST39190 Embryo, 9 week Homo sapiens cDNA 5' end), AA362653 (EST72375 Namalwa B cells I Homo sapiens cDNA 5' end), and AA829841 (od40d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1370401 3' similar to WP:F10G7.1 CE02624). The predicted amino acid sequence disclosed herein for qg596_12 was searched
10 against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qg596_12 protein demonstrated at least some similarity to the sequence identified as U40029 (coded for by C. elegans cDNA yk16b1.3; coded for by C. elegans cDNA yk8g6.5; coded for by C. elegans cDNA yk8g6.3; coded for by C. elegans cDNA yk6d3.5). Based upon sequence similarity, qg596_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer
15 program predicts two potential transmembrane domains within the qg596_12 protein sequence, one centered around amino acid 180 and another around amino acid 660 of SEQ ID NO:16.

qg596_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 33 kDa was detected in membrane fractions using SDS
20 polyacrylamide gel electrophoresis.

Clone "rb649_3"

A polynucleotide of the present invention has been identified as clone "rb649_3". rb649_3 was isolated from a human fetal kidney (293 cell line) cDNA library using
25 methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rb649_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rb649_3 protein").

30 The nucleotide sequence of rb649_3 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rb649_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 42 to 54 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted

mature amino acid sequence beginning at amino acid 55. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the rb649_3 protein.

- 5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rb649_3 should be approximately 2500 bp.

 The nucleotide sequence disclosed herein for rb649_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rb649_3 demonstrated at least some similarity with sequences
10 identified as AA177001 (nc01h02.s1 NCL_CGAP_Pr1 Homo sapiens cDNA clone IMAGE 182). The predicted amino acid sequence disclosed herein for rb649_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted rb649_3 protein demonstrated at least some similarity to sequences identified as AB002405 (LAK-4p [Homo sapiens]), R89470 (Collagen/TGF-beta-
15 1 fusion protein), and U23516 (Undefined [Caenorhabditis elegans]). Based upon sequence similarity, rb649_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts eight additional potential transmembrane domains within the rb649_3 protein sequence, centered around amino acids 140, 240, 280, 325, 370, 425, 475, and 540 of SEQ ID NO:18, respectively. The
20 nucleotide sequence of rb649_3 indicates that it may contain a simple GGA repeat region.

Clone "ca106_19x"

 A polynucleotide of the present invention has been identified as clone "ca106_19x". A cDNA clone was first isolated from a mouse embryonic (ES cell embryoid bodies
25 harvested 2-12 days after LIF removed) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate ca106_19x from a mixture of human fetal brain and human adult brain cDNA libraries.
30 ca106_19x is a full-length human clone, including the entire coding sequence of a secreted protein (also referred to herein as "ca106_19x protein").

 The nucleotide sequence of ca106_19x as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the ca106_19x protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ca106_19x should be approximately 4050 bp.

- 5 The nucleotide sequence disclosed herein for ca106_19x was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ca106_19x demonstrated at least some similarity with sequences identified as AA886998 (oj30g03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1499860 3'), F08279 (H. sapiens partial cDNA sequence; clone c-zpe11), F13022 (H. sapiens partial cDNA sequence; clone c-3hf07), H38128 (yp46c12.s1 Homo sapiens cDNA clone 190486 3'), T77601 (yc91e07.r1 Homo sapiens cDNA clone 23192 5'), U93720 (Homo sapiens TEX28 mRNA, complete cds), W55512 (ma28h03.r1 Life Tech mouse brain Mus musculus cDNA clone 312053 5'), and Z22333 (H.sapiens DNA sequence). The predicted amino acid sequence disclosed herein for ca106_19x was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ca106_19x protein demonstrated at least some similarity to sequences identified as U56965 (C15H9.4 gene product [Caenorhabditis elegans]) and U93720 (TEX28 [Homo sapiens]). Based upon sequence similarity, ca106_19x proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the ca106_19x protein sequence, centered around amino acids 170, 430, 590, and 625 of SEQ ID NO:20, respectively. The nucleotide sequence of ca106_19x indicates that it contains at least one repetitive element.

Clone "ci52_2"

- 25 A polynucleotide of the present invention has been identified as clone "ci52_2". A cDNA clone was first isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate ci52_2 from a human fetal brain cDNA library. ci52_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ci52_2 protein").

The nucleotide sequence of ci52_2 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the ci52_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 9 to 21 of SEQ ID NO:22 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ci52_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ci52_2 should be approximately 1775 bp.

The nucleotide sequence disclosed herein for ci52_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ci52_2 demonstrated at least some similarity with sequences identified as AA083339 (zn31d10.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 549043 5'), AA514339 (nf56c10.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 923922), AA628942 (af28f01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 1032985 3', mRNA sequence), M78692 (EST00840 Homo sapiens cDNA clone HHCMC16), N67265 (yz49d04.s1 Homo sapiens cDNA clone 286375 3'), N95514 (yy62d10.r1 Homo sapiens cDNA clone 278131 5'), Q60715 (Human brain Expressed Sequence Tag EST00840; standard; cDNA), and R46588 (yg51a12.s1 Homo sapiens cDNA clone 35984 3'). The predicted amino acid sequence disclosed herein for ci52_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ci52_2 protein demonstrated at least some similarity to the sequence identified as M68866 (stranded at second [Drosophila melanogaster]). Based upon sequence similarity, ci52_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the ci52_2 protein sequence, one around amino acid 146 and another around amino acid 177 of SEQ ID NO:22.

Clone "md124_16"

A polynucleotide of the present invention has been identified as clone "md124_16". A cDNA clone was first isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then

used to isolate md124_16 from a human adult kidney cDNA library. md124_16 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "md124_16 protein").

The nucleotide sequence of md124_16 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the md124_16 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino acids 152 to 164 of SEQ ID NO:24 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 165. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the md124_16 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone md124_16 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for md124_16 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. md124_16 demonstrated at least some similarity with sequences identified as AA215643 (zr98d05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683721 3'), AA489121 (aa56b07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824917 5'), W72865 (zd59e07.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344964 3'), and W76100 (zd59e07.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344964 5'). Based upon sequence similarity, md124_16 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of md124_16 indicates that it may contain at least one MER repeat sequence.

Clone "pk366_7"

A polynucleotide of the present invention has been identified as clone "pk366_7". pk366_7 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pk366_7 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pk366_7 protein").

The nucleotide sequence of pk366_7 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pk366_7 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Amino acids 361 to 373 of SEQ ID NO:26 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 374. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pk366_7 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pk366_7 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for pk366_7 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pk366_7 demonstrated at least some similarity with sequences identified as AA057428 (zf57c11.s1 Soares retina N2b4HR Homo sapiens cDNA clone 381044 3'), AA457625 (aa89e09.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 838504 5'), AA601545 (nn87h11.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1098213), T19564 (Human gene signature HUMGS00629; standard; cDNA to mRNA), and U94831 (Homo sapiens multispinning membrane protein mRNA, complete cds). The predicted amino acid sequence disclosed herein for pk366_7 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pk366_7 protein demonstrated at least some similarity to sequences identified as D87444 (endomembrane protein EMP70 precursor isolog [Arabidopsis thaliana]), U94831 (multispinning membrane protein [Homo sapiens]), and U95973 (endomembrane protein EMP70 precursor isolog [Arabidopsis thaliana]). Based upon sequence similarity, pk366_7 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts nine additional potential transmembrane domains within the pk366_7 protein sequence, centered around amino acids 191, 260, 288, 325, 355, 412, 447, 481, and 517 of SEQ ID NO:26, respectively.

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Clone "pl741_5"

A polynucleotide of the present invention has been identified as clone "pl741_5". pl741_5 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No.

5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pl741_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pl741_5 protein").

5 The nucleotide sequence of pl741_5 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pl741_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28. Amino acids 3 to 15 of SEQ ID NO:28 are a predicted leader/signal sequence, with the predicted
10 mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pl741_5 protein.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pl741_5 should be approximately 3000 bp.

 The nucleotide sequence disclosed herein for pl741_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pl741_5 demonstrated at least some similarity with sequences identified as AA283176 (zt17a04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
20 clone 713358 3'), AA204801 (zq61d12.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 646103 5'), and H59410 (yr19g04.r1 Homo sapiens cDNA clone 205782 5'). The predicted amino acid sequence disclosed herein for pl741_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pl741_5 protein demonstrated at least some similarity to
25 sequences identified as U00027 (Cdc23p cell cycle protein [*Saccharomyces cerevisiae*]) and U58763 (F10C5.1 [*Caenorhabditis elegans*]). Based upon sequence similarity, pl741_5 proteins and each similar protein or peptide may share at least some activity. Analysis of the amino acid sequence of the predicted pl741_5 protein reveals the presence of four TPR (tetratricopeptide) domains. TPR domains are found in a wide variety of proteins with
30 varying functions and localizations — from the nucleus to the extracellular milieu — and are thought to function as protein-protein interaction domains. The TPR domains are found at amino acid residues 166-194, 328-356, 362-390, and 396-424 of SEQ ID NO:28.

Clone "pp314_19"

A polynucleotide of the present invention has been identified as clone "pp314_19". pp314_19 was isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pp314_19 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pp314_19 protein").

The nucleotide sequence of pp314_19 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pp314_19 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 147 to 159 of SEQ ID NO:30 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 160; amino acids 238 to 250 of SEQ ID NO:30 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 251. Due to the hydrophobic nature of these possible leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the pp314_19 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pp314_19 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pp314_19 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pp314_19 demonstrated at least some similarity with sequences identified as AA044042 (zk58g05.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 487064 5', mRNA sequence), AA127902 (zl12d01.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 501697 5'), AA609481 (af14a12.s1 Soares testis NHT Homo sapiens cDNA clone 1031614 3', mRNA sequence), T26699 (Human gene signature HUMGS08949; standard; cDNA to mRNA), and W93399 (zd95b06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 357203 3'). The predicted amino acid sequence disclosed herein for pp314_19 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pp314_19 protein demonstrated at least some similarity to sequences identified as AE000857 (chaperonin [Methanobacterium thermoautotrophicum]), AJ006549 (ThsA [Pyrodicticum occultum]), and L34691 (thermophilic factor 56 [Sulfolobus shibatae]). Based upon sequence

similarity, pp314_19 proteins and each similar protein or peptide may share at least some activity. Analysis of the amino acid sequence of the predicted pp314_19 protein revealed the cpn60_TCP1 signature (at amino acids 29-570 of SEQ ID NO:30) which has some ATPase activity and is indicative of chaperonins. A P-loop motif — a common motif in
5 ATP- and GTP-binding proteins — is found around amino acid 200 of SEQ ID NO:30. The presence of the P-loop is interesting when taken in conjunction with the potential ATPase activity associated with the cpn60_TCP1 signature. The TopPredII computer program predicts three additional potential transmembrane domains within the pp314_19 protein sequence, centered around amino acids 55, 90, and 330 of SEQ ID NO:30,
10 respectively.

pp314_19 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 6 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15 Clone "pv35_1"

A polynucleotide of the present invention has been identified as clone "pv35_1". pv35_1 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
20 analysis of the amino acid sequence of the encoded protein. pv35_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pv35_1 protein").

The nucleotide sequence of pv35_1 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper
25 reading frame and the predicted amino acid sequence of the pv35_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pv35_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pv35_1 was searched against the
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pv35_1 demonstrated at least some similarity with sequences identified as AA335869 (EST40348 Epididymus Homo sapiens cDNA 5' end), AA599418 (ag23c03.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1071172 3'), and H03595

(yj42e06.r1 Homo sapiens cDNA clone 151426 5'). The predicted amino acid sequence disclosed herein for pv35_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pv35_1 protein demonstrated at least some similarity to sequences identified as Z99277 (Y53C12A.3 [Caenorhabditis elegans]). Based upon sequence similarity, pv35_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the pv35_1 protein sequence, centered around amino acids 127, 161, 192, and 250 of SEQ ID NO:32, respectively.

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Clone "pw337_6"

A polynucleotide of the present invention has been identified as clone "pw337_6". pw337_6 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pw337_6 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pw337_6 protein").

The nucleotide sequence of pw337_6 as presently determined is reported in SEQ ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pw337_6 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Another potential pw337_6 reading frame and predicted amino acid sequence is encoded by basepairs 648 to 908 of SEQ ID NO:33 and is reported in SEQ ID NO:238. The overlapping reading frames of SEQ ID NO:34 and SEQ ID NO:238 could be joined if a frameshift were introduced into the nucleotide sequence of SEQ ID NO:33 between position 645 and position 736.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pw337_6 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for pw337_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pw337_6 demonstrated at least some similarity with sequences identified as AA682471 (zj18c02.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 450626 3', mRNA sequence), T20708 (Human gene signature HUMGS01925;

standard; cDNA to mRNA), W24658 (zb63b05.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 308241 5'), and Z82192 (Homo sapiens DNA sequence from PAC 186O1 on chromosome 22). The predicted amino acid sequence disclosed herein for pw337_6 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pw337_6 protein demonstrated at least some similarity to the sequence identified as Z82192 (dJ186O1.1 [Homo sapiens]). Based upon sequence similarity, pw337_6 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pw337_6 protein sequence centered around amino acid 75 of SEQ ID NO:34. The nucleotide sequence of pw337_6 indicates that it may contain one or more repetitive elements.

pw337_6 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 22 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "rd610_1"

A polynucleotide of the present invention has been identified as clone "rd610_1". rd610_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rd610_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rd610_1 protein").

The nucleotide sequence of rd610_1 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rd610_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rd610_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for rd610_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rd610_1 demonstrated at least some similarity with sequences identified as AA442056 (zw56f08.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774087 5'), AA992905 (ot92b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens

cDNA clone IMAGE 1624211 3', mRNA sequence), D31767 (Human mRNA for KIAA0058 gene, complete cds), and T40090 (Human Serrate-1 (HJ1) cDNA; standard; cDNA). Based upon sequence similarity, rd610_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential
5 transmembrane domain within the rd610_1 protein sequence centered around amino acid 30 of SEQ ID NO:36; amino acids 23 to 35 of SEQ ID NO:36 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 36.

rd610_1 protein was expressed in a COS cell expression system, and an expressed
10 protein band of approximately 7 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "rd810_6"

A polynucleotide of the present invention has been identified as clone "rd810_6".
15 rd810_6 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rd810_6 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to
20 herein as "rd810_6 protein").

The nucleotide sequence of rd810_6 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rd810_6 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Amino
25 acids 112 to 124 of SEQ ID NO:38 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 125. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the rd810_6 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rd810_6 should be approximately 850 bp.

The nucleotide sequence disclosed herein for rd810_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rd810_6 demonstrated at least some similarity with sequences

identified as AA452718 (zx39d04.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788839 5', mRNA sequence), AA292888 (zt66c01.r1 Soares testis NHT Homo sapiens cDNA clone 727296 5'), and T23348 (Human gene signature HUMGS05169; standard; cDNA to mRNA). Based upon sequence similarity, rd810_6 proteins and each similar
5 protein or peptide may share at least some activity.

rd810_6 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

10 Clone "cf85_1"

A polynucleotide of the present invention has been identified as clone "cf85_1". A cDNA clone was first isolated from a human adult placenta library cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis
15 of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate cf85_1 from a human adult brain cDNA library. cf85_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cf85_1 protein").

The nucleotide sequence of cf85_1 as presently determined is reported in SEQ ID
20 NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cf85_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cf85_1 should be approximately 2000 bp.

25 The nucleotide sequence disclosed herein for cf85_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cf85_1 demonstrated at least some similarity with sequences identified as H50932 (yo35f03.r1 Homo sapiens cDNA clone 179933 5'), H51595 (yo35f03.s1 Homo sapiens cDNA clone 179933 3'), and T24664 (Human gene signature
30 HUMGS06728; standard; cDNA to mRNA). Based upon sequence similarity, cf85_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the cf85_1 protein sequence, centered around amino acids 150, 195, and 220 of SEQ ID NO:40,

respectively. The nucleotide sequence of cf85_1 indicates that it may contain an Alu repetitive element.

Clone "dd504_18"

5 A polynucleotide of the present invention has been identified as clone "dd504_18". dd504_18 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dd504_18 is a full-length
10 clone, including the entire coding sequence of a secreted protein (also referred to herein as "dd504_18 protein").

The nucleotide sequence of dd504_18 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd504_18 protein
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 134 to 146 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 147. Amino acids 7 to 19 of SEQ ID NO:42 are also a possible leader/signal sequence, with a predicted mature amino acid sequence beginning in that case at amino acid 20. Due to the hydrophobic
20 nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the dd504_18 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dd504_18 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for dd504_18 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dd504_18 demonstrated at least some similarity with sequences identified as AA393779 (zt77f07.r1 Soares testis NHT Homo sapiens cDNA clone 728389 5' similar to WP:F41E7.1 CE03301; mRNA sequence), AA429420 (zw51f02.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773595 5' similar to WP W02B12.7 CE03767
30 KINENSIN-LIKE PROTEIN), AC002038 (** SEQUENCING IN PROGRESS ** Human chromosome 16p12 BAC clone CIT987SK-101B6; HTGS phase 1, 1 unordered pieces; Homo sapiens chromosome 2 clone 101B6 from 2p11, complete sequence), H10672 (yl99g09.r1 Homo sapiens cDNA clone 46448 5'), and R59895 (yh07f12.r1 Homo sapiens cDNA clone 42477 5'). The predicted amino acid sequence disclosed herein for dd504_18

was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dd504_18 protein demonstrated at least some similarity to sequences identified as AE000854 (Na⁺/H⁺-exchanging protein Na⁺/H⁺ antiporter [Methanobacterium thermoautotrophicum]) and Z68106 (F41E7.1 [Caenorhabditis elegans]). Based upon sequence similarity, dd504_18 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts eight potential transmembrane domains within the dd504_18 protein sequence, centered around amino acids 20, 48, 118, 144, 191, 220, 268, and 326 of SEQ ID NO:42, respectively.

- 10 dd504_18 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 36 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "np26_3"

- 15 A polynucleotide of the present invention has been identified as clone "np26_3". np26_3 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. np26_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to
20 herein as "np26_3 protein").

- The nucleotide sequence of np26_3 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the np26_3 protein
25 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone np26_3 should be approximately 3800 bp.

- The nucleotide sequence disclosed herein for np26_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
30 FASTA search protocols. np26_3 demonstrated at least some similarity with sequences identified as AA118527 (mo99d08.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone 567855 5'), AA284633 (zt15d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713191 3', mRNA sequence), AA427620 (zw30d02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770787 3' similar to contains MER17.b1 MER17

repetitive element; mRNA sequence), and AA496955 (aa42f01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 823609 3', mRNA sequence). The predicted amino acid sequence disclosed herein for np26_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted np26_3 protein demonstrated at least some similarity to the sequence identified as M86752 (transformation-sensitive protein [Homo sapiens]). Based upon sequence similarity, np26_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the np26_3 protein sequence centered around amino acid 146 of SEQ ID NO:44.

np26_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 63 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "pm412_12"

A polynucleotide of the present invention has been identified as clone "pm412_12". pm412_12 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm412_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm412_12 protein").

The nucleotide sequence of pm412_12 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm412_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 607 to 619 of SEQ ID NO:46 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 620. Due to the hydrophobic nature of this possible leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the pm412_12 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm412_12 should be approximately 4000 bp.

The nucleotide sequence disclosed herein for pm412_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. pm412_12 demonstrated at least some similarity with sequences identified as AA176820 (zp34a12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 611326 3'), AA425762 (zw47f10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773227 3' similar to TR:G285999 G285999 ORF, COMPLETE CDS), AA568580 (nm21a10.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1060794 similar to TR:G642306 G642306 HYPOTHETICAL 153.8 KD PROTEIN), AA610863 (np98h01.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE 1142449 similar to TR G285999 G285999 ORF, COMPLETE CDS), AA769312 (nz39f06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 1290179 similar to TR Q15393 Q15393 ORF, COMPLETE CDS; mRNA sequence), D13642 (Human mRNA for KIAA0017 gene, complete cds), and T92977 (ye22e09.r1 Homo sapiens cDNA clone 118504 5'). The predicted amino acid sequence disclosed herein for pm412_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pm412_12 protein demonstrated at least some similarity to sequences identified as AF043699 (ORF; similar to human UV-damaged DNA binding factor [C. elegans]), D13642 (KIAA0017 [Homo sapiens]), R72386 (XAP-1, part of the DNA repair complex), and X54413 (alpha1(IX) collagen precursor [Homo sapiens]). Based upon sequence similarity, pm412_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the pm412_12 protein sequence, centered around amino acids 277, 415, and 1060 of SEQ ID NO46, respectively.

pm412_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 119 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "pm421_3"

A polynucleotide of the present invention has been identified as clone "pm421_3". pm421_3 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm421_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm421_3 protein").

The nucleotide sequence of pm421_3 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm421_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 10 to 22 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pm421_3 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm421_3 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for pm421_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm421_3 demonstrated at least some similarity with sequences identified as AA196485 (zq59a06.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 645874 3'), AA421712 (zu26g11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 739172 5', mRNA sequence), AC005026 (Homo sapiens clone GS489L14; HTGS phase 1, 3 unordered pieces), AC005028 (Homo sapiens clone GS539F22; HTGS phase 1, 1 unordered pieces), Q60534 (Human brain Expressed Sequence Tag EST02540; standard; cDNA), and R13985 (yf68h04.r1 Homo sapiens cDNA clone 27722 5'). Based upon sequence similarity, pm421_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the pm421_3 protein sequence centered around amino acid 36 of SEQ ID NO:48.

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Clone "pv6_1"

A polynucleotide of the present invention has been identified as clone "pv6_1". pv6_1 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pv6_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pv6_1 protein").

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The nucleotide sequence of pv6_1 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pv6_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50. Amino acids 39 to 51 of SEQ ID NO:50 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 52. Amino acids 8 to 20 of SEQ ID NO:50 are also a possible leader/signal sequence, with a predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the pv6_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pv6_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pv6_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pv6_1 demonstrated at least some similarity with sequences identified as B53192 (CIT-HSP-2009D9.TR CIT-HSP Homo sapiens genomic clone 2009D9, genomic survey sequence), R18429 (yg02g05.r1 Homo sapiens cDNA clone 31056 5'), T77089 (yc93b02.r1 Homo sapiens cDNA clone 23653 5'), and X89480 (S.scrofa mRNA for membrane protein). The predicted amino acid sequence disclosed herein for pv6_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pv6_1 protein demonstrated at least some similarity to the sequence identified as X89480 (transmembrane protein [Sus scrofa]). Based upon sequence similarity, pv6_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pv6_1 protein sequence centered around amino acid 21 of SEQ ID NO:50.

Clone "qs14_3"

A polynucleotide of the present invention has been identified as clone "qs14_3". A cDNA clone was isolated from a human whole embryo cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate qs14_3 from a human fetal heart cDNA library. qs14_3 is a full-length

clone, including the entire coding sequence of a secreted protein (also referred to herein as "qs14_3 protein").

The nucleotide sequence of qs14_3 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the qs14_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 15 to 27 of SEQ ID NO:52 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should
10 the predicted leader/signal sequence not be separated from the remainder of the qs14_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qs14_3 should be approximately 5000 bp.

The nucleotide sequence disclosed herein for qs14_3 was searched against the
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qs14_3 demonstrated at least some similarity with sequences identified as AA558554 (nl69g02.s1 NCI_CGAP_Pr4.1 Homo sapiens cDNA clone IMAGE 1045970 similar to TR G307329 G307329 PROTOCADHERIN 43), AB002343 (Human mRNA for KIAA0345 gene), and L43592 (Rattus norvegicus protocadherin-3 (pcdh3)
20 mRNA, and translated products). The predicted amino acid sequence disclosed herein for qs14_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qs14_3 protein demonstrated at least some similarity to sequences identified as AF029343 (protocadherin [Homo sapiens]), AF042192 (protocadherin [Xenopus]), AF052685 (protocadherin 43 [Homo sapiens]),
25 L11373 (protocadherin 43 [Homo sapiens]), R49144 (Product of alternative splicing of human protocadherin-43 mRNA), and Y08715 (protocadherin [Mus musculus]). The cadherins are a family of calcium-binding membrane glycoproteins. Most cadherins are capable of acting as cell adhesion molecules (CAMs). Motif analysis of the predicted qs14_3 protein also detects the 'cadherins extracellular repeated domain signature'. Based
30 upon sequence similarity, qs14_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the qs14_3 protein sequence, one centered around amino acid 510 and another around amino acid 721 of SEQ ID NO:52.

qs14_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 132 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5 Clone "qy338_9"

A polynucleotide of the present invention has been identified as clone "qy338_9". qy338_9 was isolated from a human adult blood (promyelocytic leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on
10 the basis of computer analysis of the amino acid sequence of the encoded protein. qy338_9 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qy338_9 protein").

The nucleotide sequence of qy338_9 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the qy338_9 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 144 to 156 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 157. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qy338_9 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qy338_9 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for qy338_9 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qy338_9 demonstrated at least some similarity with sequences identified as AA205412 (zq66a09.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 646552 3' similar to contains Alu repetitive element; contains element LTR1 repetitive element; mRNA), AA595068 (no40h10.s1 NCI_CGAP_Pr23 Homo sapiens
30 cDNA clone IMAGE 1103203 similar to WP C27F2.4 CE01171 METHYLTRANSFERASE), AJ224442 (Homo sapiens mRNA for putative methyltransferase), and H40834 (yo05g09.r1 Homo sapiens cDNA clone 177088 5'). The predicted amino acid sequence disclosed herein for qy338_9 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qy338_9 protein

demonstrated at least some similarity to sequences identified as AJ224442 (methyltransferase [Homo sapiens]), U40419 (similar to *S. cerevisiae* gene YCR47C, putative 30.7 kd methyltransferase (SP YCT7_YEAST,P25627) [*Caenorhabditis elegans*]), and Z69240 (putative methyltransferase [*S. cerevisiae*]). Based upon sequence similarity, qy338_9
5 proteins and each similar protein or peptide may share at least some activity.

qy338_9 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 34 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

10 Clone "rc58_1"

A polynucleotide of the present invention has been identified as clone "rc58_1". rc58_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
15 analysis of the amino acid sequence of the encoded protein. rc58_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rc58_1 protein").

The nucleotide sequence of rc58_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper
20 reading frame and the predicted amino acid sequence of the rc58_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 2 to 14 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should
25 the predicted leader/signal sequence not be separated from the remainder of the rc58_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rc58_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for rc58_1 was searched against the
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rc58_1 demonstrated at least some similarity with sequences identified as AA203670 (zx52d04.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 446119 5' similar to gb X07868_rna1 PUTATIVE INSULIN-LIKE GROWTH FACTOR II ASSOCIATED (HUMAN); mRNA sequence), AA878778 (oe80h01.s1

NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1417969 3', mRNA sequence), and U96448 (Bos taurus cleavage and polyadenylation specificity factor 30 kDa subunit mRNA, complete cds). The predicted amino acid sequence disclosed herein for rc58_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the
5 BLASTX search protocol. The predicted rc58_1 protein demonstrated at least some similarity to sequences identified as AF033201 (cleavage and polyadenylation specificity factor [Mus musculus]) and U96448 (cleavage and polyadenylation specificity factor 30 kDa subunit [Bos taurus]). Based upon sequence similarity, rc58_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer
10 program predicts an additional potential transmembrane domain within the rc58_1 protein sequence centered around amino acid 53 of SEQ ID NO:56.

Clone "rd232_5"

A polynucleotide of the present invention has been identified as clone "rd232_5".
15 rd232_5 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rd232_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as
20 "rd232_5 protein").

The nucleotide sequence of rd232_5 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rd232_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rd232_5 should be approximately 3800 bp.

The nucleotide sequence disclosed herein for rd232_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rd232_5 demonstrated at least some similarity with sequences
30 identified as AA768103 (oc16g01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1341072), AA831487 (oc61a11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354172 3', mRNA sequence), and R57296 (F2616 Fetal heart Homo sapiens cDNA clone F2616 5' end). The predicted amino acid sequence disclosed herein for rd232_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the

BLASTX search protocol. The predicted rd232_5 protein demonstrated at least some similarity to the sequence identified as Z79755 (F43G9.2 [Caenorhabditis elegans]). Based upon sequence similarity, rd232_5 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential
5 transmembrane domain within the rd232_5 protein sequence centered around amino acid 225 of SEQ ID NO:58. The nucleotide sequence of rd232_5 indicates that it may contain a simple AC repeat region.

Clone "ck213_12"

10 A polynucleotide of the present invention has been identified as clone "ck213_12". ck213_12 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ck213_12 is a full-length
15 clone, including the entire coding sequence of a secreted protein (also referred to herein as "ck213_12 protein").

The nucleotide sequence of ck213_12 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ck213_12 protein
20 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ck213_12 should be approximately 3500 bp.

The nucleotide sequence disclosed herein for ck213_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. ck213_12 demonstrated at least some similarity with sequences identified as AA062731 (zm01h03.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone 512885 3' similar to TR:G1136390 G1136390 KIAA0164 PROTEIN, mRNA sequence), AA173803 (zp30f05.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 610977 3', mRNA sequence), D79986 (Human mRNA for KIAA0164 protein
30 gene, complete cds), and R01411 (ye77c11.s1 Homo sapiens cDNA clone 123764 3'). The predicted amino acid sequence disclosed herein for ck213_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ck213_12 protein demonstrated at least some similarity to the sequence identified as D79986 (similar to human DNA-binding protein 5 [Homo sapiens],

KIAA0164 protein [Homo sapiens], HUMKIAA04_1). Based upon sequence similarity, ck213_12 proteins and each similar protein or peptide may share at least some activity.

Clone "pg195_1"

5 A polynucleotide of the present invention has been identified as clone "pg195_1". pg195_1 was isolated from a human adult thyroid cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pg195_1 is a full-length clone,
10 including the entire coding sequence of a secreted protein (also referred to herein as "pg195_1 protein").

The nucleotide sequence of pg195_1 as presently determined is reported in SEQ ID NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pg195_1 protein
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pg195_1 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for pg195_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
20 FASTA search protocols. pg195_1 demonstrated at least some similarity with sequences identified as H72617 (yu02g10.r1 Homo sapiens cDNA clone 232674 5') and W37280 (zc11a07.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321972 5', mRNA sequence). The predicted amino acid sequence disclosed herein for pg195_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the
25 BLASTX search protocol. The predicted pg195_1 protein demonstrated at least some similarity to the sequence identified as AF007270 (contains similarity to myosin heavy chain [Arabidopsis thaliana]). Based upon sequence similarity, pg195_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the pg195_1 protein
30 sequence, one centered around amino acid 480 and another around amino acid 520 of SEQ ID NO:62. The nucleotide sequence of pg195_1 indicates that it may contain one or more repetitive sequences.

Clone "pw460_5"

A polynucleotide of the present invention has been identified as clone "pw460_5". pw460_5 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pw460_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pw460_5 protein").

The nucleotide sequence of pw460_5 as presently determined is reported in SEQ ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pw460_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64. Amino acids 17 to 29 of SEQ ID NO:64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pw460_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pw460_5 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pw460_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pw460_5 demonstrated at least some similarity with sequences identified as AA447258 (zw93e03.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784540 5', mRNA sequence), AA617801 (nq04f05.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE 1142913), AC002486 (Human BAC clone RG367O17 from 7p15-p21, complete sequence), AC004837 (human genomic DNA fragments), and H45347 (yo65h03.r1 Homo sapiens cDNA clone 182837 5'). Based upon sequence similarity, pw460_5 proteins and each similar protein or peptide may share at least some activity.

30 Clone "qa136_1"

A polynucleotide of the present invention has been identified as clone "qa136_1". qa136_1 was isolated from a human adult cartilage (chondrosarcoma HTB-94 line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on

the basis of computer analysis of the amino acid sequence of the encoded protein. qa136_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qa136_1 protein").

The nucleotide sequence of qa136_1 as presently determined is reported in SEQ ID NO:65. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qa136_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:66. Amino acids 15 to 27 of SEQ ID NO:66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qa136_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qa136_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for qa136_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qa136_1 demonstrated at least some similarity with sequences identified as AA758023 (ah67g02.s1 Soares testis NHT Homo sapiens cDNA clone 1320722 3', mRNA sequence), R69911 (yi47c02.r1 Homo sapiens cDNA clone 142370 5'), and T21835 (Human gene signature HUMGS03376; standard; cDNA to mRNA). Based upon sequence similarity, qa136_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the qa136_1 protein sequence, centered around amino acids 59, 136, 171, 201, and 268 of SEQ ID NO:66, respectively.

qa136_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "qy1261_2"

A polynucleotide of the present invention has been identified as clone "qy1261_2". qy1261_2 was isolated from a human adult blood (promyelocytic Leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein.

qy1261_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qy1261_2 protein").

The nucleotide sequence of qy1261_2 as presently determined is reported in SEQ ID NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the qy1261_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68. Amino acids 100 to 112 of SEQ ID NO:68 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 113. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
10 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qy1261_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qy1261_2 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for qy1261_2 was searched against the
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qy1261_2 demonstrated at least some similarity with sequences identified as AA076472 (zm91b06.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 545267 5'), AA115700 (zl87g10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 511650 5', mRNA sequence), and AA190522 (zp85e07.r1 Stratagene HeLa cell
20 s3 937216 Homo sapiens cDNA clone 627012 5'). The predicted amino acid sequence disclosed herein for qy1261_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qy1261_2 protein demonstrated at least some similarity to the sequence identified as U49082 (transporter protein [Homo sapiens]). Based upon sequence similarity, qy1261_2 proteins and each
25 similar protein or peptide may share at least some activity. The TopPredII computer program predicts ten additional potential transmembrane domains within the qy1261_2 protein sequence, centered around amino acids 80, 157, 203, 227, 286, 322, 365, 403, 426, and 462 of SEQ ID NO:68. The nucleotide sequence of qy1261_2 indicates that it may contain one or more Alu repeat sequences.

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Clone "rd432_4"

A polynucleotide of the present invention has been identified as clone "rd432_4". rd432_4 was isolated from a human kidney (293 embryonal carcinoma cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S.

Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rd432_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rd432_4 protein").

5 The nucleotide sequence of rd432_4 as presently determined is reported in SEQ ID NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rd432_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:70.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rd432_4 should be approximately 2200 bp.

15 The nucleotide sequence disclosed herein for rd432_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rd432_4 demonstrated at least some similarity with sequences identified as AA662913 (nu92b03.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1218125, mRNA sequence). Based upon sequence similarity, rd432_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the rd432_4 protein sequence, which includes amino acids 102-122 of SEQ ID NO:70. The nucleotide sequence of rd432_4 indicates that it may contain one or more Alu repetitive elements.

20 rd432_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 18 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "rb789_14"

25 A polynucleotide of the present invention has been identified as clone "rb789_14". rb789_14 was isolated from a human kidney (293 embryonal carcinoma line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rb789_14
30 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rb789_14 protein").

 The nucleotide sequence of rb789_14 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rb789_14 protein

corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:72. Amino acids 9 to 21 of SEQ ID NO:72 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain
5 should the predicted leader/signal sequence not be separated from the remainder of the rb789_14 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rb789_14 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for rb789_14 was searched against the
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rb789_14 demonstrated at least some similarity with sequences identified as AL008582 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 223H9; HTGS phase 1), AL022393 (Homo sapiens DNA sequence from P1 p373c6 on chromosome 6p21.31-21.33. Contains zinc finger proteins, pseudogenes, ESTs
15 and STS), N28823 (yx71f11.r1 Homo sapiens cDNA clone 267213 5'), and Q60944 (Human brain Expressed Sequence Tag EST01025; standard; DNA). Based upon sequence similarity, rb789_14 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the rb789_14 protein sequence, one centered around
20 amino acid 30 and another around amino acid 75 of SEQ ID NO:72.

Clone "yd137_1"

A polynucleotide of the present invention has been identified as clone "yd137_1". yd137_1 was isolated from a human adult brain cDNA library and was identified as
25 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd137_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd137_1 protein").

The nucleotide sequence of yd137_1 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper
30 reading frame and the predicted amino acid sequence of the yd137_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 27 to 39 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 40. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain

should the predicted leader/signal sequence not be separated from the remainder of the yd137_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd137_1 should be approximately 789 bp.

5 The nucleotide sequence disclosed herein for yd137_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd137_1 demonstrated at least some similarity with sequences identified as AI015619 (ov29g02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638770 3' similar to WP:C34B2.10 CE16898; mRNA sequence). The predicted
10 amino acid sequence disclosed herein for yd137_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yd137_1 protein demonstrated at least some similarity to the sequence identified as AF043693 (Caenorhabditis elegans cosmid C34B2). Based upon sequence similarity, yd137_1 proteins and each similar protein or peptide may share at least some
15 activity. The TopPredII computer program predicts two additional potential transmembrane domains within the yd137_1 protein sequence, one centered around amino acid 30 and another around amino acid 55 of SEQ ID NO:74.

Clone "yd218_1"

20 A polynucleotide of the present invention has been identified as clone "yd218_1". yd218_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd218_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd218_1 protein").

25 The nucleotide sequence of yd218_1 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd218_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76. Amino acids 2 to 14 of SEQ ID NO:76 are a predicted leader/signal sequence, with the predicted
30 mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yd218_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd218_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for yd218_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd218_1 demonstrated at least some similarity with sequences identified as AA402818 (zu55f06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741923 3', mRNA sequence) and AI150344 (qf35b11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751997 3', mRNA sequence). Based upon sequence similarity, yd218_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the yd218_1 protein sequence, one centered around amino acid 66 and another around amino acid 100 of SEQ ID NO:76.

yd218_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 15 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "ye11_1"

A polynucleotide of the present invention has been identified as clone "ye11_1". ye11_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye11_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye11_1 protein").

The nucleotide sequence of ye11_1 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ye11_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye11_1 should be approximately 2700 bp.

The nucleotide sequence disclosed herein for ye11_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ye11_1 demonstrated at least some similarity with sequences identified as AC005082 (** SEQUENCING IN PROGRESS ** Homo sapiens clone RG271G13; HTGS phase 1, 7 unordered pieces). The predicted amino acid sequence disclosed herein for ye11_1 was searched against the GenPept and GeneSeq amino acid

sequence databases using the BLASTX search protocol. The predicted ye11_1 protein demonstrated at least some similarity to sequences identified as AF059569 (actin binding protein MAYVEN [Homo sapiens]) and R94386 (Human neural cell protein marker RR/B). MAYVEN is an actin-binding protein expressed in brain. Hidden markov model
5 analysis reveals the presence of a BTB (BR-c/Ttk) domain in the predicted ye11_1 protein. BTB domains are characteristic of certain bacterial membrane transport proteins. The MAYVEN protein is thought to contain a similar BTB motif, an indication that ye11_1 and MAYVEN may share a similar function. Based upon sequence similarity, ye11_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII
10 computer program predicts two potential transmembrane domains within the ye11_1 protein sequence, one centered around amino acid 20 and another around amino acid 480 of SEQ ID NO:78.

ye11_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 57 kDa was detected in conditioned medium and
15 membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "ye72_1"

A polynucleotide of the present invention has been identified as clone "ye72_1". ye72_1 was isolated from a human fetal brain cDNA library and was identified as
20 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye72_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye72_1 protein").

The nucleotide sequence of ye72_1 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper
25 reading frame and the predicted amino acid sequence of the ye72_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino acids 24 to 36 of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 37. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should
30 the predicted leader/signal sequence not be separated from the remainder of the ye72_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye72_1 should be approximately 2261 bp.

The nucleotide sequence disclosed herein for ye72_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ye72_1 demonstrated at least some similarity with sequences identified as AA968450 (op49d06.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
5 IMAGE:1580171 3', mRNA sequence). The predicted amino acid sequence disclosed herein for ye72_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ye72_1 protein demonstrated at least some similarity to sequences identified as U16258 (I kappa BR [Homo sapiens]) and W15483 (Human P28). Based upon sequence similarity, ye72_1 proteins and each
10 similar protein or peptide may share at least some activity. Hidden markov model analysis reveals the presence of three ankyrin repeats in the predicted ye72_1 protein at amino acids 273 to 306, 307 to 339, and 341 to 373 of SEQ ID NO:80. The ankyrin 33-residue repeating motif, an L-shaped structure with protruding beta-hairpin tips, mediates specific macromolecular interactions with cytoskeletal, membrane, and regulatory proteins. The
15 TopPredII computer program predicts an additional potential transmembrane domain within the ye72_1 protein sequence centered around amino acid 140 of SEQ ID NO:80.

Clone "ye78_1"

A polynucleotide of the present invention has been identified as clone "ye78_1".
20 ye78_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye78_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye78_1 protein").

The nucleotide sequence of ye78_1 as presently determined is reported in SEQ ID
25 NO:81, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ye78_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:82. Amino acids 78 to 90 of SEQ ID NO:82 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 91. Amino acids 42 to 54 are also a possible
30 leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 55. Due to the hydrophobic nature of leader/signal sequences, both of these predicted and possible leader sequences are likely to act as a transmembrane domain should either of them not be separated from the remainder of the ye78_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye78_1 should be approximately 2654 bp.

The nucleotide sequence disclosed herein for ye78_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
5 FASTA search protocols. ye78_1 demonstrated at least some similarity with sequences identified as AA522797 (ni40c10.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:979314, mRNA sequence). Based upon sequence similarity, ye78_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer
10 program predicts four potential transmembrane domains within the ye78_1 protein sequence, centered around amino acids 55, 75, 84, and 480 of SEQ ID NO:12, respectively.

Clone "ye90_1"

A polynucleotide of the present invention has been identified as clone "ye90_1". ye90_1 was isolated from a human fetal brain cDNA library and was identified as
15 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye90_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye90_1 protein").

The nucleotide sequence of ye90_1 as presently determined is reported in SEQ ID NO:83, and includes a poly(A) tail. What applicants presently believe to be the proper
20 reading frame and the predicted amino acid sequence of the ye90_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:84. Amino acids 7 to 19 of SEQ ID NO:84 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should
25 the predicted leader/signal sequence not be separated from the remainder of the ye90_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye90_1 should be approximately 1505 bp.

The nucleotide sequence disclosed herein for ye90_1 was searched against the
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ye90_1 demonstrated at least some similarity with sequences identified as AI079268 (oz32f06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1677059 3', mRNA sequence) and T25543 (Human gene signature HUMGS07715, standard; cDNA to mRNA). Based upon sequence similarity, ye90_1

proteins and each similar protein or peptide may share at least some activity. Motifs analysis reveals the presence of a neutral zinc metallopeptidases, zinc-binding region signature beginning around amino acid residue 236 of SEQ ID NO:84; some known secreted proteins have this motif. The TopPredII computer program predicts two
5 additional potential transmembrane domains within the ye90_1 protein sequence, one centred around amino acid 195 and another around amino acid 300 of SEQ ID NO:84.

Clone "yi62_1"

A polynucleotide of the present invention has been identified as clone "yi62_1".
10 yi62_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yi62_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yi62_1 protein").

The nucleotide sequence of yi62_1 as presently determined is reported in SEQ ID
15 NO:85, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yi62_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:86. Amino acids 2 to 14 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal
20 sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yi62_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yi62_1 should be approximately 1240 bp.

The nucleotide sequence disclosed herein for yi62_1 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yi62_1 demonstrated at least some similarity with sequences identified as R57572 (F3589 Fetal heart Homo sapiens cDNA clone F3589 5' end, mRNA sequence). Based upon sequence similarity, yi62_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four
30 potential transmembrane domains within the yi62_1 protein sequence, centered around amino acids 15, 75, 100, and 125 of SEQ ID NO:86, respectively.

Clone "yk78_1"

A polynucleotide of the present invention has been identified as clone "yk78_1". yk78_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk78_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk78_1 protein").

The nucleotide sequence of yk78_1 as presently determined is reported in SEQ ID NO:87, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk78_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:88. Amino acids 57 to 69 of SEQ ID NO:88 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 70. Amino acids 7 to 19 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of leader/signal sequences, both of these predicted and possible leader sequences are likely to act as a transmembrane domain should either of them not be separated from the remainder of the yk78_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk78_1 should be approximately 1088 bp.

The nucleotide sequence disclosed herein for yk78_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk78_1 demonstrated at least some similarity with sequences identified as AC004921 (** SEQUENCING IN PROGRESS ** Homo sapiens clone DJ0899E09; HTGS phase 1, 11 unordered pieces). Based upon sequence similarity, yk78_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the yk78_1 protein sequence, one centered around amino acid 20 and another around amino acids 60 of SEQ ID NO:88.

Clone "yk251_1"

A polynucleotide of the present invention has been identified as clone "yk251_1". yk251_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk251_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk251_1 protein").

The nucleotide sequence of yk251_1 as presently determined is reported in SEQ ID NO:89, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk251_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:90. Amino acids 17 to 29 of SEQ ID NO:90 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk251_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk251_1 should be approximately 2558 bp.

The nucleotide sequence disclosed herein for yk251_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the databases. The TopPredII computer program predicts a potential transmembrane domain within the yk251_1 protein sequence centered, around amino acid 20 of SEQ ID NO:90. The nucleotide sequence of yk251_1 indicates that it may contain Alu and SVA repetitive elements.

Clone "yt14_1"

20 A polynucleotide of the present invention has been identified as clone "yt14_1". yt14_1 was isolated from a human adult retina (WERI-Rb1 retinoblastoma line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yt14_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to
25 herein as "yt14_1 protein").

The nucleotide sequence of yt14_1 as presently determined is reported in SEQ ID NO:91, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yt14_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:92. Amino acids 1 to 9 are
30 a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 10. Due to the hydrophobic nature of this possible leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk251_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yt14_1 should be approximately 2429 bp.

The nucleotide sequence disclosed herein for yt14_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yt14_1 demonstrated at least some similarity with sequences identified as W07167 (za93b12.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 300095 5', mRNA sequence). The predicted amino acid sequence disclosed herein for yt14_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yt14_1 protein demonstrated at least some similarity to the sequence identified as AF002196 (weak similarity to Bacillus and Pseudomonas probable glucarate transporters (GI 709999 and PIR S27616) [Caenorhabditis elegans]). Based upon sequence similarity, yt14_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the yt14_1 protein sequence, centered around amino acids 10, 40, 65, 90, 130, and 160 of SEQ ID NO:92, respectively. The nucleotide sequence of yt14_1 indicates that it may contain Alu and L1 repetitive elements.

Clone "bf157_16"

A polynucleotide of the present invention has been identified as clone "bf157_16". bf157_16 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bf157_16 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "bf157_16 protein").

The nucleotide sequence of bf157_16 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bf157_16 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bf157_16 should be approximately 3480 bp.

The nucleotide sequence disclosed herein for bf157_16 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bf157_16 demonstrated at least some similarity with sequences identified as AA186595 (zo71g04.r1 Stratagene pancreas (#937208) Homo sapiens cDNA

clone 592374 5' similar to WP C16A3.3 CE04004 HUMAN ALPHA-FETOPROTEIN ENHANCER-BINDING PROTEIN), AA630405 (ac09b05.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 855921 3' similar to WP C16A3.3 CE04004 HUMAN ALPHA-FETOPROTEIN ENHANCER-BINDING PROTEIN; mRNA sequence), AF075104
5 (Homo sapiens full length insert cDNA YR39H06), H49655 (yq20h07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 274428 3'), Z28494 (H. sapiens partial cDNA sequence; clone 22G07; version 1; strand(-), single read), Z56794 (H.sapiens CpG island DNA genomic MseI fragment, clone), and Z64553 (H.sapiens CpG island DNA genomic MseI fragment, clone 139f5, forward read cpg139f5.ft1a). The predicted amino acid
10 sequence disclosed herein for bf157_16 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bf157_16 protein demonstrated at least some similarity to sequences identified as R23962 (AFP-1. DNA encoding protein binding to alpha-fetoprotein gene enhancer -useful for prodn. of biological active protein), and U41534 (similar to yeast hypothetical protein
15 (SP:YB9M_YEAST,P38344); similar to human alpha-fetoprotein enhancer-binding protein (PIR:A41948) [Caenorhabditis elegans]). Based upon sequence similarity, bf157_16 proteins and each similar protein or peptide may share at least some activity. Hidden Markov model and motifs analyses have revealed the presence of the following protein domains in the predicted bf157_16 protein: four Zinc finger, C2H2 type, domains at
20 amino acids 4 to 28, 67 to 91, 252 to 275, and 303 to 330 of SEQ ID NO:94; and a D-isomer-specific 2-hydroxyacid dehydrogenases signature at residues 119 to 131 of SEQ ID NO:94. A number of NAD-dependent 2-hydroxyacid dehydrogenases, with at least some specificity for the D-isomer of their substrate, have been shown to be functionally and structurally related. Clone bf157_16 appears to encode a novel protein which may have
25 NAD-dependent 2-hydroxyacid dehydrogenase activity.

bf157_16 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 16 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

30 Clone "bk343_2"

A polynucleotide of the present invention has been identified as clone "bk343_2". bk343_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer

analysis of the amino acid sequence of the encoded protein. bk343_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bk343_2 protein").

5 The nucleotide sequence of bk343_2 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bk343_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96.

Another possible reading frame within the bk343_2 clone extends from nucleotide 45 to nucleotide 188 of SEQ ID NO:95, and encodes the amino acid sequence reported in
10 SEQ ID NO:239. Amino acids 5 to 17 of SEQ ID NO:239 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:239.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bk343_2 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for bk343_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bk343_2 demonstrated at least some similarity with sequences
20 identified as AA156969 (zo51d05.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 590409 5'), AA947938 (oe60c08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1416014 3', mRNA sequence), N31147 (yx52g05.r1 Homo sapiens cDNA clone 265400 5'), N42759 (yy22a09.r1 Homo sapiens cDNA clone 271960 5'), N47537 (yy90h10.s1 Homo sapiens cDNA clone 280867 3'), R68913 (yi43b04.r1 Homo sapiens
25 cDNA clone 141967 5'), T24885 (Human gene signature HUMGS06991; standard; cDNA to mRNA), and T30099 (EST112339 Homo sapiens cDNA 5' end similar to None). The predicted amino acid sequence disclosed herein for bk343_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bk343_2 protein demonstrated at least some similarity to sequences
30 identified as Z72508 (F28H7.4 [Caenorhabditis elegans]) and Z78417 (C35C5.3 [Caenorhabditis elegans]). Based upon sequence similarity, bk343_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the bk343_2 protein sequence centered around amino acid 36 of SEQ ID NO:96.

Clone "cd205_2"

A polynucleotide of the present invention has been identified as clone "cd205_2". cd205_2 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cd205_2 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "cd205_2 protein").

The nucleotide sequence of cd205_2 as presently determined is reported in SEQ ID NO:97, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cd205_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98. Amino acids 92 to 104 of SEQ ID NO:98 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 105. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cd205_2 protein.

Another possible reading frame within the cd205_2 clone extends from nucleotide 59 to nucleotide 478 of SEQ ID NO:97, and encodes the amino acid sequence reported in SEQ ID NO:240. The open reading frames encoding the amino acid sequences of SEQ ID NO:98 and SEQ ID NO:240 could be joined if one or more frame shifts were made in the nucleotide sequence of SEQ ID NO:97.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cd205_2 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for cd205_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cd205_2 demonstrated at least some similarity with sequences identified as AA053543 (zl71f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 510091 5' similar to gb:M77830 DESMOPLAKIN I AND II (HUMAN)), AC005332 (Homo sapiens chromosome 17, clone hRPK.147_L_13, complete sequence), N84944 (J1677F Homo sapiens cDNA clone J1677 5' similar to CHROMOSOME 4 (CLONE P4-661) STS4-563), N86274 (J7481F Fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7481 5' similar to CHROMOSOME 4 (CLONE P4-661) STS4-563), W68823 (zd37f04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342847 5', mRNA sequence), and Z54387 (H.sapiens CpG island DNA genomic MseI fragment, clone 10g3, reverse read cpg10g3.rt1a). Based upon sequence similarity, cd205_2 proteins and each similar protein

or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cd205_2 protein sequence located around amino acid 105 of SEQ ID NO:98.

5 Clone "cw1292_8"

A polynucleotide of the present invention has been identified as clone "cw1292_8". cw1292_8 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. cw1292_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw1292_8 protein").

The nucleotide sequence of cw1292_8 as presently determined is reported in SEQ ID NO:99, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the cw1292_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:100. Amino acids 18 to 30 of SEQ ID NO:100 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cw1292_8 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1292_8 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for cw1292_8 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1292_8 demonstrated at least some similarity with sequences identified as AA017976 (mh46h10.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus), AA423855 (zv79c04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 759846 3'), AA626784 (ad09f08.s1 Soares NbHFB Homo sapiens cDNA clone 877767 3', mRNA
30 sequence), H23387 (ym57f05.r1 Homo sapiens cDNA clone 52337 5'), H78534 (yu13d06.r1 Homo sapiens cDNA clone 233675 5'), H79021 (yu13d06.s1 Homo sapiens cDNA clone 233675 3'), R44807 (yg23g06.s1 Homo sapiens cDNA clone 33217 3'), T24772 (Human gene signature HUMGS06848; standard; cDNA to mRNA), T97424 (ye53h08.r1 Homo sapiens cDNA clone 121503 5'), and Z44597 (H. sapiens partial cDNA sequence; clone c-25a05).

The predicted amino acid sequence disclosed herein for cw1292_8 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1292_8 protein demonstrated at least some similarity to the sequence identified as M33521 (HLA-B-associated transcript 3 (BAT3) [Homo]). Based upon sequence similarity, cw1292_8 proteins and each similar protein or peptide may share at least some activity.

Clone "cw1475_2"

A polynucleotide of the present invention has been identified as clone "cw1475_2". cw1475_2 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw1475_2 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "cw1475_2 protein").

The nucleotide sequence of cw1475_2 as presently determined is reported in SEQ ID NO:101, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw1475_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:102.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1475_2 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for cw1475_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1475_2 demonstrated at least some similarity with sequences identified as AA527429 (ng41a10.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937338, mRNA sequence), AD000092 (Homo sapiens DNA from chromosome 19p13.2 cosmid R31240, R30272 and R28549 containing the EKLF, GCDH, CRTCL, and RAD23A genes, genomic sequence), H98508 (yv90f08.r1 Homo sapiens cDNA clone 250023 5'), N25554 (yx76f08.s1 Homo sapiens cDNA clone 267687 3'), N50970 (yy94b06.s1 Homo sapiens cDNA clone 281171 3'), N81188 (yw36g06.r1 Homo sapiens cDNA clone 254362 5'), R32569 (yh54g03.r1 Homo sapiens cDNA clone 133588 5'), R81017 (yi94g02.r1 Homo sapiens cDNA clone 146930 5' similar to contains Alu repetitive element; contains MER30 repetitive element), T06537 (EST04426 Homo sapiens cDNA clone HFB083 similar to EST containing Alu repeat), T31594 (Probe (BLUR11) for Alu repeat sequence), and W30895 (zb78e12.r1 Soares senescent fibroblasts NbHSF Homo). Based upon sequence similarity, cw1475_2 proteins and each similar protein or peptide may share at

least some activity. The nucleotide sequence of cw1475_2 indicates that it may contain one or more of the following repetitive elements: Alu, SVA.

Clone "dd428_4"

5 A polynucleotide of the present invention has been identified as clone "dd428_4". dd428_4 was isolated from a human adult testes cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dd428_4 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "dd428_4 protein").

10 The nucleotide sequence of dd428_4 as presently determined is reported in SEQ ID NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd428_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
15 dd428_4 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for dd428_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dd428_4 demonstrated at least some similarity with sequences identified as AC000057 (Human BAC clone RG067M09 from 7q21-7q22; HTGS phase 3, complete sequence), AC005500 (complete sequence), L27428 (Human L1 putative reverse transcriptase gene insertion in hamster, 3'end), T86176 (y78c11.s1 Homo sapiens cDNA clone 114356 3' similar to gb L25879 EPOXIDE HYDROLASE (HUMAN); contains L1 repetitive element), X61307 (Staphylococcus aureus spa gene for protein A), and Z69647 (Human DNA sequence from cosmid E118G4, maps to 10cen and 11q13-q14). Based upon
20 sequence similarity, dd428_4 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of dd428_4 indicates that it may contain L1 repeat sequences.

Clone "dh1073_12"

30 A polynucleotide of the present invention has been identified as clone "dh1073_12". dh1073_12 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dh1073_12 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "dh1073_12 protein").

The nucleotide sequence of dh1073_12 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dh1073_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106.

- 5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dh1073_12 should be approximately 2400 bp.

The nucleotide sequence disclosed herein for dh1073_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dh1073_12 demonstrated at least some similarity with sequences
10 identified as AA257983 (zs35h03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 687221 3' similar to TR G666014 G666014 SA SA GENE PRODUCT, COMPLETE CDS PRECURSOR; mRNA sequence), AA526325 (ni59g06.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone 981178 similar to contains Alu repetitive element), AF001549 (Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence), N57823 (yv59e04.s1
15 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 247038 3'), and N68408 (za13c05.s1 Homo sapiens cDNA clone 292424 3'). The predicted amino acid sequence disclosed herein for cw1292_8 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dh1073_12 protein demonstrated at least some similarity to the sequence identified as AC003034 (Gene with
20 similarity to rat kidney-specific (KS) gene [Homo sapiens]). Based upon sequence similarity, dh1073_12 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of dh1073_12 indicates that it may contain an Alu repetitive element.

25 Clone "dw78_1"

A polynucleotide of the present invention has been identified as clone "dw78_1". dw78_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
30 analysis of the amino acid sequence of the encoded protein. dw78_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dw78_1 protein").

The nucleotide sequence of dw78_1 as presently determined is reported in SEQ ID NO:107, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the dw78_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:108.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dw78_1 should be approximately 1400 bp.

5 The nucleotide sequence disclosed herein for dw78_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dw78_1 demonstrated at least some similarity with sequences identified as AA807622 (nv65g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 1234724, mRNA sequence), AF086326 (Homo sapiens full length insert cDNA
10 clone ZD54A02), D37980 (Dictyostelium discoideum DDCOF1 gene for cofilin, complete cds (exon1-2)), H26207 (yl53c04.r1 Homo sapiens cDNA clone 161958 5'), N72717 (za47h03.s1 Homo sapiens cDNA clone 295733 3' similar to contains Alu repetitive element; contains element L1 repetitive element), T23963 (Human gene signature HUMGS05917; standard; cDNA to mRNA), U14567 (**ALU WARNING Human Alu-J
15 subfamily consensus sequence), U43572 (Human alpha-N-acetylglucosaminidase (NAGLU) gene, complete cds), W42787 (zc25a04.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 323310 3'), and W73472 (zd54a02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344426 3', mRNA sequence). The predicted amino acid sequence disclosed herein for dw78_1 was searched against the GenPept and
20 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dw78_1 protein demonstrated at least some similarity to the sequence identified as D32202 (alpha 1C adrenergic receptor isoform 2 [Homo sapiens]). Based upon sequence similarity, dw78_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential
25 transmembrane domains within the dw78_1 protein sequence, one centered around amino acid 45 and another around amino acid 93 of SEQ ID NO:108. The nucleotide sequence of dw78_1 indicates that it may contain an Alu repetitive element.

Clone "fh116_11"

30 A polynucleotide of the present invention has been identified as clone "fh116_11". fh116_11 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fh116_11 is a full-length

clone, including the entire coding sequence of a secreted protein (also referred to herein as "fh116_11 protein").

The nucleotide sequence of fh116_11 as presently determined is reported in SEQ ID NO:109, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the fh116_11 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:110.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fh116_11 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for fh116_11 was searched against the
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fh116_11 demonstrated at least some similarity with sequences identified as AA054185 (zf51c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone 380458 5'), AA057975 (mj57b02.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 480171 5' similar to WP:F57A8.2 CE05983), AA128902 (zn90a05.s1 Stratagene
15 lung carcinoma 937218 Homo sapiens cDNA clone 565424 3'), AA426021 (zw49h09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773441 3'), AA505926 (nh98g03.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone 966580), AI079540 (oz04e08.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674374 3' similar to WP:F57A8.2 CE05983; mRNA sequence), H68794 (yr91h09.s1 Homo sapiens
20 cDNA clone 212705 3'), H86659 (yt02c04.r1 Homo sapiens cDNA clone 223110 5'), T24554 (Human gene signature HUMGS06604; standard; cDNA to mRNA), U96490 (Rattus norvegicus liver mRNA, complete cds), and W00635 (yy71d12.r1 Homo sapiens cDNA clone 278999 5' similar to contains element PTR5 repetitive element). The predicted amino acid sequence disclosed herein for fh116_11 was searched against the GenPept and
25 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fh116_11 protein demonstrated at least some similarity to sequences identified as AF004876 (54TMp [Homo sapiens]), U96490 (unknown [Rattus norvegicus]), and Z70781 (F57A8.2 [Caenorhabditis elegans]). Based upon sequence similarity, fh116_11 proteins and each similar protein or peptide may share at least some activity. The
30 TopPredII computer program predicts five potential transmembrane domains within the fh116_11 protein sequence, centered around amino acids 35 to 49, 136, 171, 215, and 270 of SEQ ID NO:110, respectively.

fh116_11 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 28 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5 Clone "fy356_14"

A polynucleotide of the present invention has been identified as clone "fy356_14". fy356_14 was isolated from a human fetal placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. fy356_14 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fy356_14 protein").

The nucleotide sequence of fy356_14 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the fy356_14 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 385 to 397 of SEQ ID NO:112 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 398. Due to the hydrophobic nature of this possible leader/signal sequence, it is likely to act as a
20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fy356_14 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fy356_14 should be approximately 3700 bp.

The nucleotide sequence disclosed herein for fy356_14 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fy356_14 demonstrated at least some similarity with sequences identified as AA017639 (ze38c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone 361256 5' similar to PIR S55385 S55385 PEA-15 protein - mouse), AA181529 (zp51f07.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 612997 3'), AA687129
30 (nv63d03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 1234469), AA811277 (ob68e06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336546, mRNA sequence), N53623 (yz04e01.r1 Homo sapiens cDNA clone 282072 5'), T25935 (Human gene signature HUMGS08167; standard; cDNA to mRNA), T24538 (Human gene signature HUMGS06585; standard; cDNA to mRNA), and X86809 (H.sapiens mRNA for

major astrocytic phosphoprotein PEA-15). The predicted amino acid sequence disclosed herein for fy356_14 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fy356_14 protein demonstrated at least some similarity to the sequence identified as X86809 (PEA-15 gene product [Homo sapiens]). Based upon sequence similarity, fy356_14 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the fy356_14 protein sequence, centered around amino acid 398 of SEQ ID NO:112.

10 Clone "iw66_1"

A polynucleotide of the present invention has been identified as clone "iw66_1". iw66_1 was isolated from a human adult retina (WERI-Rb1 retinoblastoma line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. iw66_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "iw66_1 protein").

The nucleotide sequence of iw66_1 as presently determined is reported in SEQ ID NO:113, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the iw66_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:114. Amino acids 9 to 21 of SEQ ID NO:114 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the iw66_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone iw66_1 should be approximately 1450 bp.

The nucleotide sequence disclosed herein for iw66_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. iw66_1 demonstrated at least some similarity with sequences identified as AA216917 (mv75h11.r1 Soares mouse 3NME12 5 Mus musculus cDNA clone 660933 5'), AA339406 (EST44484 Fetal brain I Homo sapiens cDNA 5' end), AI275861 (ql68b12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1877471 3', mRNA

sequence), Q61257 (Human brain Expressed Sequence Tag EST01278; standard; DNA), R89651 (ym97c08.r1 Homo sapiens cDNA clone 166862 5'), W53584 (md55f06.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 372323 5'), and Z60886 (H.sapiens CpG island DNA genomic MseI fragment, clone 38a8, reverse read
5 cpg38a8.rt1a). The predicted amino acid sequence disclosed herein for iw66_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted iw66_1 protein demonstrated at least some similarity to sequences identified as AF004874 (latent TGF-beta binding protein-2 [Mus musculus]), L29029 (amino acid feature Rod protein domain, aa 266 468; amino acid
10 feature globular protein domain, aa 32..265 [Chlamydomonas reinhardtii]), R27150 (PspA fragment), and R79478 (Mouse LTBP-2). Based upon sequence similarity, iw66_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the iw66_1 protein sequence, centered around amino acids 45, 74, and 158 of SEQ ID NO:114,
15 respectively. The nucleotide sequence of iw66_1 indicates that it may contain one or more of the following repetitive elements: MIR.

Clone "kh13_4"

A polynucleotide of the present invention has been identified as clone "kh13_4".
20 kh13_4 was isolated from a human adult testes cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. kh13_4 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "kh13_4 protein").

The nucleotide sequence of kh13_4 as presently determined is reported in SEQ ID
25 NO:115, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the kh13_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:116.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone kh13_4 should be approximately 950 bp.

30 The nucleotide sequence disclosed herein for kh13_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. kh13_4 demonstrated at least some similarity with sequences identified as AA435981 (zu01f08.s1 Soares testis NHT Homo sapiens cDNA clone 730599 3'), AA436078 (zu01f08.r1 Soares testis NHT Homo sapiens cDNA clone 730599 5'),

AA778636 (af87c04.s1 Soares testis NHT Homo sapiens cDNA clone 1048998 3' similar to gb:M94856 PSORIASIS-ASSOCIATED FATTY ACID BINDING PROTEIN HOMOLOG (HUMAN); mRNA sequence), M94856 (Human fatty acid binding protein homologue (PA-FABP) mRNA, complete cds), and Q66842 (Melanogenic inhibitor; standard; DNA).

- 5 The predicted amino acid sequence disclosed herein for kh13_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted kh13_4 protein demonstrated at least some similarity to sequences identified as M94856 (fatty acid binding protein homologue [Homo sapiens]) and R55866 (Melanogenic inhibitor). Fatty acid binding protein homologue (M94856) is described as
- 10 "a novel keratinocyte protein (psoriasis-associated fatty acid-binding protein [PA-FABP]) that is highly up-regulated in psoriatic skin and that shares similarity to fatty acid-binding proteins." Based upon sequence similarity, kh13_4 proteins and each similar protein or peptide may share at least some activity.

15 Clone "ko258_4"

- A polynucleotide of the present invention has been identified as clone "ko258_4". ko258_4 was isolated from a human adult uterus cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ko258_4 is a full-length clone, including the entire coding sequence
- 20 of a novel protein (also referred to herein as "ko258_4 protein").

The nucleotide sequence of ko258_4 as presently determined is reported in SEQ ID NO:117, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ko258_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:118.

- 25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ko258_4 should be approximately 2500 bp.

- The nucleotide sequence disclosed herein for ko258_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ko258_4 demonstrated at least some similarity with sequences
- 30 identified as AC002401 (**SEQUENCING IN PROGRESS** Homo sapiens chromosome 17, clone RPC875H18; HTGS phase 1, 4 unordered pieces), AC002401 (Homo sapiens chromosome 17, clone RPC875H18, complete sequence), C15329 (Human fetal brain cDNA 5'-end GEN-133H10, mRNA sequence), AF035306 (Homo sapiens clone 23771 mRNA sequence), and R28382 (IMAGE 3p clone). Based upon sequence similarity,

ko258_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the ko258_4 protein sequence, centered around amino acid 28 of SEQ ID NO:118.

5 Clone "kv10_8"

A polynucleotide of the present invention has been identified as clone "kv10_8". kv10_8 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. kv10_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "kv10_8 protein").

The nucleotide sequence of kv10_8 as presently determined is reported in SEQ ID NO:119, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the kv10_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:120.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone kv10_8 should be approximately 4300 bp.

The nucleotide sequence disclosed herein for kv10_8 was searched against the
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. kv10_8 demonstrated at least some similarity with sequences identified as AA418842 (zw01e12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 768046 3'), AC004228 (** SEQUENCING IN PROGRESS ** Homo sapiens Chromosome 11q12 pac pDJ519o3; HTGS phase 1, 18 unordered pieces), AF052108 (Homo sapiens clone
25 23687 mRNA sequence), R00761 (ye78b11.s1 Homo sapiens cDNA clone 123837 3'), T83434 (yd46b04.r1 Homo sapiens cDNA clone 111247 5'), T84080 (yd46b04.s1 Homo sapiens cDNA clone 111247 3'), and U00594 (Mustela vison unknown mRNA down regulated by TGF-beta, partial sequence). Based upon sequence similarity, kv10_8 proteins and each similar protein or peptide may share at least some activity. The
30 TopPredII computer program predicts a potential transmembrane domain within the kv10_8 protein sequence, centered around amino acids 35 to 45 of SEQ ID NO:120. The nucleotide sequence of kv10_8 indicates that it may contain one or more of the following repetitive elements: Alu, SVA.

Clone "LL89_3"

A polynucleotide of the present invention has been identified as clone "LL89_3". LL89_3 was isolated from a human adult thyroid cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. LL89_3 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "LL89_3 protein").

The nucleotide sequence of LL89_3 as presently determined is reported in SEQ ID NO:121, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the LL89_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:122.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone LL89_3 should be approximately 900 bp.

The nucleotide sequence disclosed herein for LL89_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. LL89_3 demonstrated at least some similarity with sequences identified as AL031010 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 422F24, complete sequence), H78002 (yu82h09.r1 Homo sapiens cDNA clone 240353 5'), and W90018 (zh72c08.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417614 3'). Based upon sequence similarity, LL89_3 proteins and each similar protein or peptide may share at least some activity.

Clone "mc300_1"

A polynucleotide of the present invention has been identified as clone "mc300_1". mc300_1 was isolated from a human adult thyroid cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. mc300_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "mc300_1 protein").

The nucleotide sequence of mc300_1 as presently determined is reported in SEQ ID NO:123, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the mc300_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:124.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mc300_1 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for mc300_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. mc300_1 demonstrated at least some similarity with sequences identified as AA142942 (IMAGE 3p clone), AA315222 (EST187017 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end), AA142942 (zl43c04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 504678 3'), AI246503 (qn64a06.x1 NCI_CGAP_HN4 Homo sapiens cDNA clone IMAGE:1902994 3', mRNA sequence), D61461 (Human fetal brain cDNA 5'-end GEN-404B08), D79662 (Human aorta cDNA 5'-end GEN-300D05, mRNA sequence), H93575 (yv14h11.s1 Homo sapiens cDNA clone 242757 3'), T25928 (Human gene signature HUMGS08160; standard; cDNA to mRNA), and W93059 (zd93h06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 357083 3'). Based upon sequence similarity, mc300_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of mc300_1 indicates that it may contain one or more Alu repetitive elements.

15

Clone "ml227_1"

A polynucleotide of the present invention has been identified as clone "ml227_1". ml227_1 was isolated from a human adult brain (caudate nucleus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ml227_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml227_1 protein").

The nucleotide sequence of ml227_1 as presently determined is reported in SEQ ID NO:125, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml227_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:126.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml227_1 should be approximately 2700 bp.

The nucleotide sequence disclosed herein for ml227_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml227_1 demonstrated at least some similarity with sequences identified as AA857826 (oe88e05.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1418720 3', mRNA sequence), F18464 (H.sapiens EST sequence (017-T4-16) from

skeletal muscle), H30845 (yo78d11.r1 Homo sapiens cDNA clone 184053 5'), T06839 (EST04728 Homo sapiens cDNA clone HFBDZ66), T19759 (Human gene signature HUMGS00834), T26021 (Human gene signature HUMGS08257; standard; cDNA to mRNA), and Z69043 (H.sapiens mRNA translocon-associated protein delta subunit precursor). The predicted amino acid sequence disclosed herein for ml227_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ml227_1 protein demonstrated at least some similarity to the sequence identified as Z69664 (K04D7.5 [Caenorhabditis elegans]). Based upon sequence similarity, ml227_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the ml227_1 protein sequence, centered around amino acids 465, 510, 560, 572, 595, and 615 of SEQ ID NO:126, respectively.

Clone "mm367_6"

A polynucleotide of the present invention has been identified as clone "mm367_6". mm367_6 was isolated from a human adult retina (WERI-Rb1 retinoblastoma line) cDNA library and was identified as encoding a protein. mm367_6 is a full-length clone, including the entire coding sequence of a protein (also referred to herein as "mm367_6 protein").

The nucleotide sequence of mm367_6 as presently determined is reported in SEQ ID NO:127, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the mm367_6 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:128.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mm367_6 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for mm367_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. mm367_6 demonstrated at least some similarity with sequences identified as AA114127 (zn65f02.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 563067 5'), AA127284 (zn91c12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 565558 5'), AA173842 (zp30d01.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 610945 5'), AF000364 (Homo sapiens heterogeneous nuclear ribonucleoprotein R mRNA, complete CDs), N31934 (yy22d10.s1 Homo sapiens cDNA clone 271987 3'), T24354 (Human gene signature HUMGS06385; standard; cDNA to

mRNA), U48271 (Dictyostelium discoideum UbpA deubiquitinase mRNA, complete CDs), W16579 (zb13g11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 301988 5'), and W72461 (zd67f06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 345731 3'). The predicted amino acid sequence disclosed herein for mm367_6 was searched
5 against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted mm367_6 protein demonstrated at least some similarity to sequences identified as AF000364 (heterogeneous nuclear ribonucleoprotein R [Homo sapiens]) and W26553 (Human heterogeneous nuclear ribonucleoprotein (hnRNP) A2). Based upon sequence similarity, mm367_6 proteins and each similar protein or peptide
10 may share at least some activity.

mm367_6 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 79 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15 Clone "mt124_3"

A polynucleotide of the present invention has been identified as clone "mt124_3". mt124_3 was isolated from a human adult testes cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. mt124_3 is a full-length clone, including the entire coding sequence
20 of a novel protein (also referred to herein as "mt124_3 protein").

The nucleotide sequence of mt124_3 as presently determined is reported in SEQ ID NO:129, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the mt124_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:130.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mt124_3 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for mt124_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. mt124_3 demonstrated at least some similarity with sequences
30 identified as AA435386 (ve15h01.r1 Soares mouse NbMH Mus musculus cDNA clone 818257 5' similar to TR:E198756 E198756 PUTATIVE ORF), AI185116 (qe51g07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE 1742556 3' similar to TR Q92564 Q92564 MYELOBLAST KIAA0276 ; mRNA sequence), C03847 (Human Heart cDNA, clone 3NHC2256), N74186 (za76h03.s1 Homo sapiens cDNA clone 298517 3'),

- T24234 (Human gene signature HUMGS06248; standard; cDNA to mRNA), W87997 (mf65b06.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 419123 5'), and Z86062 (Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs, polymorphic CA repeat, CpG island, CpG island genomic fragments). The predicted amino acid sequence disclosed herein for mt124_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted mt124_3 protein demonstrated at least some similarity to sequences identified as AL024499 (H38K22.2 [Caenorhabditis elegans]) and D87466 (Similar to S.cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens]).
- Based upon sequence similarity, mt124_3 proteins and each similar protein or peptide may share at least some activity.

Clone "nf56_3"

- A polynucleotide of the present invention has been identified as clone "nf56_3". nf56_3 was isolated from a human adult brain (substantia nigra) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nf56_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nf56_3 protein").

- The nucleotide sequence of nf56_3 as presently determined is reported in SEQ ID NO:131, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nf56_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:132. Amino acids 3 to 15 of SEQ ID NO:132 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the nf56_3 protein.

- The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nf56_3 should be approximately 5000 bp.

The nucleotide sequence disclosed herein for nf56_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. nf56_3 demonstrated at least some similarity with sequences

identified as H08054 (yl86a09.s1 Homo sapiens cDNA clone 44915 3'), Q60495 (Human brain Expressed Sequence Tag EST02500; standard; cDNA), T25509 (Human gene signature HUMGS07678), W34534 (mc58h01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 352753 5'), and Z64987 (H.sapiens CpG island DNA genomic MseI
5 fragment, clone 186b1, reverse read cpg186b1.rt1b). The predicted amino acid sequence disclosed herein for nf56_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted nf56_3 protein demonstrated at least some similarity to sequences identified as D86983 (similar to D.melanogaster peroxidase (U11052) [Homo sapiens]), R25079 (Drosophila SLIT protein
10 involved in axon pathway development), and X53959 (slit protein [Drosophila melanogaster]). Based upon sequence similarity, nf56_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the nf56_3 protein sequence, one centered around amino acid 514 and another around amino acid 628 of SEQ ID NO:132.

15

Clone "qy442_2"

A polynucleotide of the present invention has been identified as clone "qy442_2". qy442_2 was isolated from a human adult blood (promyelocytic leukemia HL-60 line) cDNA library using methods which are selective for cDNAs encoding secreted proteins
20 (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qy442_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qy442_2 protein").

The nucleotide sequence of qy442_2 as presently determined is reported in SEQ
25 ID NO:133, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qy442_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:134. Amino acids 3 to 15 of SEQ ID NO:134 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the
30 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qy442_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qy442_2 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for qy442_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qy442_2 demonstrated at least some similarity with sequences identified as AI081522 (on04e12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone
5 IMAGE:1555726 3' similar to contains Alu repetitive element; mRNA sequence) and AA449854 (zx37a06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788626 5'). Based upon sequence similarity, qy442_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the qy442_2 protein sequence, centered around amino acid
10 68 of SEQ ID NO:20. The nucleotide sequence of qy442_2 indicates that it may contain one or more Alu repetitive elements.

Clone "rj214_14"

A polynucleotide of the present invention has been identified as clone "rj214_14".
15 rj214_14 was isolated from a human adult neural (neuroepithelioma HTB-10 line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rj214_14 is a full-length clone, including the entire coding sequence of a secreted protein
20 (also referred to herein as "rj214_14 protein").

The nucleotide sequence of rj214_14 as presently determined is reported in SEQ ID NO:135, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rj214_14 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:136.
25 Amino acids 3 to 15 of SEQ ID NO:136 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the rj214_14 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rj214_14 should be approximately 900 bp.

The nucleotide sequence disclosed herein for rj214_14 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rj214_14 demonstrated at least some similarity with sequences

identified as AA167035 (zp05c10.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595506 3' similar to TR:G563357 G563357 GENES RAS1, RLB1 AND RLC1; mRNA sequence), AA491109 (aa52d09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 824561 5' similar to TR G563357 G563357 GENES RAS1, RLB1 AND RLC1), and

5 AI189156 (qd04c02.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1722722 3' similar to TR:O01437 O01437 SIMILAR TO DROSOPHILA RLC1 GENE PRODUCT; mRNA sequence). The predicted amino acid sequence disclosed herein for rj214_14 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted rj214_14 protein

10 demonstrated at least some similarity to sequences identified as U97016 (similar to drosophila Rlc1 gene product (NID g563361) and *S. cerevisiae* mitochondrial 60S ribosomal protein L4 (YML4) (NID g459259) [*Caenorhabditis elegans*]), and X73219 (Rlc1). *Drosophila* Rlc1 is a basic protein that is bound to the inner face of the cell membrane. Transcription mapping and nucleotide sequence analysis reveal that Rlc1 lies in the same

15 genomic region as *Drosophila* Ras1 and shows expression patterns that are similar to those of Ras1. It has been demonstrated (Ezer *et al.*, 1994, *Dev. Dyn.* 201(2): 179-190, which is incorporated by reference herein) that during embryogenesis Ras1 transcripts are restricted mainly to the embryonic central nervous system, suggesting that the Rlc1 gene product also may have a role in these nerve cells. Based upon sequence similarity,

20 rj214_14 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the rj214_14 protein sequence, centered around amino acid 32 of SEQ ID NO:136.

rj214_14 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 22 kDa was detected in membrane fractions using SDS

25 polyacrylamide gel electrophoresis.

Clone "rk80_3"

A polynucleotide of the present invention has been identified as clone "rk80_3". rk80_3 was isolated from a human adult tumor (colorectal adenocarcinoma SW480 line)

30 cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rk80_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rk80_3 protein").

The nucleotide sequence of rk80_3 as presently determined is reported in SEQ ID NO:137, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rk80_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:138. Amino acids 6 to 18 of SEQ ID NO:138 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the rk80_3 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rk80_3 should be approximately 1096 bp.

The nucleotide sequence disclosed herein for rk80_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rk80_3 demonstrated at least some similarity with sequences identified as AA418955 (zw01c10.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 15 768018 5', mRNA sequence), AB004061 (domestic pig mRNA for STAT2, complete CDs, a signal transducer and activator of transcription), C06368 (similar to none), and U38443 (Human clone JkA3 mRNA induced upon T-cell activation, 3' end). The predicted rk80_3 protein demonstrated at least some similarity to granulocyte-colony stimulating factor (G-CSF) and interleukin-6 (IL-6). Hidden Markov model analysis has revealed the presence of an IL-6/G-CSF/mast cell growth factor (MGF) family signature at amino acids 69 to 181 of SEQ ID NO:138. This family of cytokines are glycoproteins of about 170 to 180 amino acid residues in size that contain four conserved cysteine residues involved in two disulfide bonds. rk80_3 appears to encode a novel cytokine in the IL-6/G-CSF family. 20 Based upon sequence similarity, rk80_3 proteins and each similar protein or peptide may share at least some activity.

rk80_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

30

Clone "au36_42"

A polynucleotide of the present invention has been identified as clone "au36_42". au36_42 was isolated from a human adult testes cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of

the encoded protein. au36_42 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "au36_42 protein").

The nucleotide sequence of au36_42 as presently determined is reported in SEQ ID NO:139, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the au36_42 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:140.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone au36_42 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for au36_42 was searched against the
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The nucleotide sequence of au36_42 indicates that it may contain a L1ME repetitive element.

Clone "bo549_13"

15 A polynucleotide of the present invention has been identified as clone "bo549_13". bo549_13 was isolated from a human adult retina cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bo549_13 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "bo549_13 protein").

20 The nucleotide sequence of bo549_13 as presently determined is reported in SEQ ID NO:141, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bo549_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:142. The region of SEQ ID NO:141 at nucleotides 518 and 519 may represent the border of an
25 alternatively spliced exon.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bo549_13 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for bo549_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
30 FASTA search protocols. bo549_13 demonstrated at least some similarity with sequences identified as AI261562 (qz30c06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE 2028394 3' similar to TR Q63061 Q63061 HYPOTHETICAL 4.7 KD PROTEIN; mRNA sequence) and J02649 (Rat stomach (H+,K+)-ATPase mRNA, complete cds). The predicted amino acid sequence disclosed herein for bo549_13 was searched against the GenPept and

GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bo549_13 protein demonstrated at least some similarity to sequences identified as J02649 (unknown protein [Rattus norvegicus]). Based upon sequence similarity, bo549_13 proteins and each similar protein or peptide may share at least some activity.

5

Clone "da529_3"

A polynucleotide of the present invention has been identified as clone "da529_3". da529_3 was isolated from a human fetal placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
10 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. da529_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "da529_3 protein").

The nucleotide sequence of da529_3 as presently determined is reported in SEQ
15 ID NO:143, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the da529_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:144. Amino acids 59 to 71 of SEQ ID NO:144 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 72. Due to the
20 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the da529_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone da529_3 should be approximately 1150 bp.

25 The nucleotide sequence disclosed herein for da529_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. da529_3 demonstrated at least some similarity with sequences identified as AI189911 (qd33e06.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE 1725538 3' similar to TR O42204 O42204 PUTATIVE
30 TRANSMEMBRANE PROTEIN E3-16; mRNA sequence), T35254 (EST82005 Homo sapiens cDNA 5' end similar to None), U76253 (Mus musculus E25B protein mRNA, complete cds), V43619 (Human secreted protein 19 encoding DNA), W28608 (49b1 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA), and W41628 (mc47c10.r1 Soares mouse p3NMF19). The predicted amino acid sequence disclosed herein for

da529_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted da529_3 protein demonstrated at least some similarity to sequences identified as AF03895 (E25 protein [Homo sapiens]) and W63699 (Human secreted protein 19). Based upon sequence similarity, da529_3 proteins
5 and each similar protein or peptide may share at least some activity.

Clone "dm365_3"

A polynucleotide of the present invention has been identified as clone "dm365_3". A cDNA clone was first isolated from a human adult brain cDNA library using methods
10 which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate dm365_3 from a human fetal brain cDNA library. dm365_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein
15 as "dm365_3 protein").

The nucleotide sequence of dm365_3 as presently determined is reported in SEQ ID NO:145, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dm365_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:146.
20 Amino acids 1 to 13 of SEQ ID NO:146 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 14. Amino acids 40 to 52 of SEQ ID NO:146 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 53. Due to the hydrophobic nature of each of these predicted leader/signal sequences, each predicted leader/signal
25 sequence is likely to act as a transmembrane domain should it not be separated from the remainder of the dm365_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dm365_3 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for dm365_3 was searched against the
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dm365_3 demonstrated at least some similarity with sequences identified as AC005533 (** SEQUENCING IN PROGRESS ** Homo sapiens clone DJ0794K21; HTGS phase 1, 22 unordered pieces), AI125562 (qd94d09.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE 1737137 3', mRNA sequence), R02268 (ye85c10.r1

Homo sapiens cDNA clone 124530 5' similar to contains LTR5 repetitive element), and V90427 (EST clone DM365). Based upon sequence similarity, dm365_3 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of dm365_3 indicates that it may contain repetitive sequences.

- 5 dm365_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "fa171_1"

- 10 A polynucleotide of the present invention has been identified as clone "fa171_1". fa171_1 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fa171_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "fa171_1 protein").

- 15 The nucleotide sequence of fa171_1 as presently determined is reported in SEQ ID NO:147, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fa171_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:148.

- The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 fa171_1 should be approximately 2500 bp.

- The nucleotide sequence disclosed herein for fa171_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fa171_1 demonstrated at least some similarity with sequences identified as AA446057 (zw66d04.r1 Soares testis NHT Homo sapiens cDNA clone 781159
25 5', mRNA sequence), AC002099 (** SEQUENCING IN PROGRESS ** Genomic sequence from Human 9q34; HTGS phase 1, 2 unordered pieces), AC002355 (** SEQUENCING IN PROGRESS ** Genomic sequence from Human 9q34; HTGS phase 1, 7 unordered pieces), and U10185 (Xenopus laevis XPMC2 protein mRNA, complete cds). The predicted amino acid sequence disclosed herein for fa171_1 was searched against the GenPept and
30 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fa171_1 protein demonstrated at least some similarity to sequences identified as R67549 (Fruiting body inducing polypeptide) and U10185 (XPMC2 protein [Xenopus laevis]). XPMC2 is a Xenopus cDNA clone that can rescue several different yeast mitotic catastrophe mutants defective in Wee1 kinase function, and is a nuclear protein. Based

upon sequence similarity, fa171_1 proteins and each similar protein or peptide may share at least some activity.

Clone "lp572_2"

5 A polynucleotide of the present invention has been identified as clone "lp572_2". lp572_2 was isolated from a human adult blood (peripheral blood mononuclear cells treated with granulocyte-colony stimulating factor *in vivo*) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. lp572_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "lp572_2 protein").

The nucleotide sequence of lp572_2 as presently determined is reported in SEQ ID NO:149, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the lp572_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:150. Amino acids 79 to 91 of SEQ ID NO:150 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 92. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the lp572_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone lp572_2 should be approximately 2100 bp.

The nucleotide sequence disclosed herein for lp572_2 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. lp572_2 demonstrated at least some similarity with sequences identified as AA489012 (aa56a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 824908 3'), AA533633 (nf73b09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE 925529, mRNA sequence), AC004686 (Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence), T18977 (g07030t Testis 1 Homo sapiens cDNA clone g07030 5' end),
30 T21490 (Human gene signature HUMGS02862), and W73324 (zd01h01.r1 Pancreatic Islet Homo sapiens cDNA clone 339409 5'). The predicted amino acid sequence disclosed herein for lp572_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted lp572_2 protein

demonstrated at least some similarity to sequences identified as AL03262 (predicted using Genefinder [Caenorhabditis elegans]). Based upon sequence similarity, lp572_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the
5 lp572_2 protein sequence, centered around amino acids 129, 263, 286, 326, and 378 of SEQ ID NO:150, respectively.

Clone "pe246_1"

A polynucleotide of the present invention has been identified as clone "pe246_1".
10 pe246_1 was isolated from a human adult blood (chronic myelogenous leukemia line K562) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pe246_1 is a full-length clone, including the entire coding sequence
15 of a secreted protein (also referred to herein as "pe246_1 protein").

The nucleotide sequence of pe246_1 as presently determined is reported in SEQ ID NO:151, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe246_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:152.
20 Amino acids 193 to 205 of SEQ ID NO:152 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 206. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pe246_1 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe246_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for pe246_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pe246_1 demonstrated at least some similarity with sequences
30 identified as AA234138 (zr51b06.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 666899 5' similar to SW FCEB_HUMAN Q01362 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT), AA418443 (zv92e05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 767264 5' similar to SW FCEB_RAT P13386 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT; mRNA sequence),

AC004584 (Homo sapiens chromosome 17, clone hRPC1107_A_17, complete sequence), M74509 (Human endogenous retrovirus type C oncovirus sequence), and V57903 (Hereditary haemochromatosis subregion from an HH affected individual). The predicted amino acid sequence disclosed herein for pe246_1 was searched against the GenPept and

5 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pe246_1 protein demonstrated at least some similarity to sequences identified as L35848 (IgE receptor beta subunit [Homo sapiens]), R05026 (Beta subunit of rat high affinity IgE receptor Fc(epsilon)RI), and R42341 (Subunit of the human IgE receptor). The first 359 nucleotides of SEQ ID NO:13 is similar in sequence to that of M74509 (Human

10 endogenous retrovirus type C oncovirus sequence) and also to several genomic sequences as a result. It appears that this region may be retroviral DNA that has been incorporated into the genome. Based upon sequence similarity, pe246_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the pe246_1 protein

15 sequence, centered around amino acids 86, 115, and 154 of SEQ ID NO:152, respectively.

Clone "qf122_3"

A polynucleotide of the present invention has been identified as clone "qf122_3". qf122_3 was isolated from a human adult bladder (carcinoma line 5637) cDNA library and

20 was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qf122_3 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "qf122_3 protein").

The nucleotide sequence of qf122_3 as presently determined is reported in SEQ ID NO:153. What applicants presently believe to be the proper reading frame and the

25 predicted amino acid sequence of the qf122_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:154.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qf122_3 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for qf122_3 was searched against the

30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qf122_3 demonstrated at least some similarity with sequences identified as AA206909 (zq80d10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 647923 5' similar to SW YYAF_BACSU P37518 HYPOTHETICAL 40.1 KD GTP-BINDING PROTEIN IN RPSF-SPO0J INTERGENIC REGION; mRNA sequence),

AA237053 (zs01c01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 683904 5' similar to SW YBN5_YEAST P38219 HYPOTHETICAL 44.2 KD PROTEIN IN SCO2-MRF1 INTERGENIC REGION), AA775776 (ad14e03.s1 Soares NbHFB Homo sapiens cDNA clone 878236 3' similar to TR P91917 P91917 W08E3.3; mRNA sequence), AL021878 (Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2; contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS), and N32932 (yy10a02.s1 Homo sapiens cDNA clone 270794 3' similar to SW:YBN5_YEAST P38219 HYPOTHETICAL 44.2 KD PROTEIN IN SCO2-MRF1 INTERGENIC REGION). The predicted amino acid sequence disclosed herein for qf122_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qf122_3 protein demonstrated at least some similarity to sequences identified as W48670 (Staphylococcus aureus gbpA protein), Z92773 (W08E3.3 [Caenorhabditis elegans]), and Z92773 (predicted using Genefinder; Similarity to Yeast hypothetical 44.2 KD protein, putative GTP-binding protein (SW P38219); cDNA EST EMBL D64516 comes from this gene). Based upon sequence similarity, qf122_3 proteins and each similar protein or peptide may share at least some activity. Analysis of protein motifs in SEQ ID NO:154 predicts an ATP/GTP-binding site motif A (P-loop) around amino acid 29 of SEQ ID NO:154.

20

Clone "qv538_1"

A polynucleotide of the present invention has been identified as clone "qv538_1". qv538_1 was isolated from a human adult testes (embryonal carcinoma NT2D1 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qv538_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qv538_1 protein").

The nucleotide sequence of qv538_1 as presently determined is reported in SEQ ID NO:155, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qv538_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:156. Amino acids 8 to 20 of SEQ ID NO:156 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the

hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qv538_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
5 qv538_1 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for qv538_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qv538_1 demonstrated at least some similarity with sequences identified as W44974 (zc22e11.r1 Soares senescent fibroblasts NbHSF Homo sapiens
10 cDNA clone 323084 5' similar to SW:FKB2_YEAST P32472 FK506-BINDING PROTEIN PRECURSOR; mRNA sequence), and Z62799 (H.sapiens CpG island DNA genomic MseI fragment, clone 73c8, reverse read cpg73c8.rt1a). The predicted amino acid sequence disclosed herein for qv538_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qv538_1 protein
15 demonstrated at least some similarity to sequences identified as AF04025 (FK506-binding protein [Mus musculus]) and W88556 (Secreted protein encoded by gene 23 clone HSQEO84). FK506-binding protein (or "FKBP") is the major high-affinity binding protein, in vertebrates, for the immunosuppressive drug FK506 (used to aid in organ transplantation acceptance among other indications). It exhibits peptidyl-prolyl cis-trans
20 isomerase activity (PPIase or rotamase). PPIase is an enzyme that accelerates protein folding by catalyzing the cis-trans isomerization of proline imidic peptide bonds in oligopeptides. Based upon sequence similarity, qv538_1 proteins and each similar protein or peptide may share at least some activity. Analysis of protein motifs in SEQ ID NO:156 detects an endoplasmic reticulum targeting sequence around amino acid 208. Hidden
25 Markov Model analysis detects an EF-hand calcium-binding domain at amino acids 183 to 211 of SEQ ID NO:156 (also found by motif analysis) and a FKBP-type peptidyl-prolyl cis-trans isomerase signatures/profile at amino acids 38 to 132 of SEQ ID NO:156. The nucleotide sequence of qv538_1 indicates that it may contain an Alu repetitive element.

qv538_1 protein was expressed in a COS cell expression system, and an expressed
30 protein band of approximately 24 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "ys20_1"

A polynucleotide of the present invention has been identified as clone "ys20_1". ys20_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ys20_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ys20_1 protein").

The nucleotide sequence of ys20_1 as presently determined is reported in SEQ ID NO:157, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ys20_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:158. Amino acids 41 to 53 of SEQ ID NO:158 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 54. Amino acids 121 to 133 of SEQ ID NO:158 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 134. Due to the hydrophobic nature of each of these predicted leader/signal sequences, each predicted leader/signal sequence is likely to act as a transmembrane domain should it not be separated from the remainder of the ys20_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ys20_1 should be approximately 2229 bp.

The nucleotide sequence disclosed herein for ys20_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ys20_1 demonstrated at least some similarity with sequences identified as B76357 (RPC111-15B19.TV RPC111 Homo sapiens genomic clone R-15B19, genomic survey sequence). Based upon sequence similarity, ys20_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the ys20_1 protein sequence, centered around amino acid 205 of SEQ ID NO:158. The nucleotide sequence of ys20_1 indicates that it may contain one or more mammalian transposon-like long terminal repeat elements, such as MCT1b/c.

Clone "as180_1"

A polynucleotide of the present invention has been identified as clone "as180_1". as180_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was

identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. as180_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "as180_1 protein").

5 The nucleotide sequence of as180_1 as presently determined is reported in SEQ ID NO:159. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the as180_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:160. Amino acids 168 to 180 of SEQ ID NO:160 are a predicted leader/signal sequence, with the predicted mature amino acid
10 sequence beginning at amino acid 181. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the as180_1 protein.

 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone as180_1 should be approximately 3580 bp.

15 The nucleotide sequence disclosed herein for as180_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. as180_1 demonstrated at least some similarity with sequences identified as AB018279 (Homo sapiens mRNA for KIAA0736 protein, complete cds), S47919 (p87 = transporter-like protein [cattle, mRNA]), V89585 (EST clone CR618), and
20 W28902 (53d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence). The predicted amino acid sequence disclosed herein for as180_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted as180_1 protein demonstrated at least some similarity to sequences identified as AB018279 (KIAA0736 protein [Homo sapiens]),
25 L05435 (synaptic vesicle protein 2 [Rattus norvegicus]), S47919 (p87 [Bos sp.]), and W64538 (Human liver cell clone HP01293 protein). Synaptic vesicle protein 2 (SV2) is a membrane glycoprotein specifically localized to secretory vesicles in neurons and endocrine cells (Bajjalieh, S.M. *et al.*, 1992, *Science* Aug 28; 257(5074):1271-1273, which is incorporated by reference herein). Based upon sequence similarity, as180_1 proteins and
30 each similar protein or peptide may share at least some activity. Analysis of amino acid motifs detected a sugar-transport protein signature around amino acid 264 of SEQ ID NO:160, and hidden Markov Model analysis detected a sugar-transporter amino acid profile from amino acid 153 to amino acid 741 of SEQ ID NO:160. The TopPredII

computer program predicts twelve potential transmembrane domains within the as180_1 protein sequence, centered around amino acids 181, 205, 248, 270, 308, 344, 432, 458, 605, 638, 654, and 710 of SEQ ID NO:160, respectively.

5 Deposit of Clones

Clones co62_12, lo311_8, ns197_1, pj193_5, pj317_2, pt332_1, qc297_15, qg596_12, and rb649_3 were deposited on July 29, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98825, from
10 which each clone comprising a particular polynucleotide is obtainable.

Clones ca106_19xx, ci52_2, md124_16, pk366_7, pl741_5, pp314_19, pv35_1, pw337_6, rd610_1, and rd810_6 were deposited on August 11, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession
15 number ATCC 98835, from which each clone comprising a particular polynucleotide is obtainable.

Clones cf85_1, dd504_18, np26_3, pm412_12, pm421_3, pv6_1, qs14_3, qy338_9, rc58_1, and rd232_5 were deposited on August 27, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an
20 original deposit under the Budapest Treaty and were given the accession number ATCC 98850, from which each clone comprising a particular polynucleotide is obtainable.

Clones ck213_12, pg195_1, pw460_5, qa136_1, qy1261_2, and rd432_4 were deposited on October 8, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under
25 the Budapest Treaty and were given the accession number ATCC 98918, from which each clone comprising a particular polynucleotide is obtainable.

Clones rb789_14, yd137_1, yd218_1, ye11_1, ye72_1, ye78_1, ye90_1, yi62_1, yk78_1, yk251_1, and yt14_1 were deposited on December 15, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209
30 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 207004, from which each clone comprising a particular polynucleotide is obtainable.

Clones bf157_16, bk343_2, cd205_2, cw1292_8, cw1475_2, dd428_4, dh1073_12, dw78_1, fh116_11, fy356_14, and iw66_1 were deposited on February 4, 1999 with the

American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 207088, from which each clone comprising a particular polynucleotide is obtainable.

5 Clones kh13_4, ko258_4, kv10_8, LL89_3, mc300_1, ml227_1, mm367_6, mt124_3, nf56_3, qy442_2, rj214_1, and rk80_3 were deposited on February 4, 1999 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 207089, from which each clone comprising a particular
10 polynucleotide is obtainable.

Clones au36_42, bo549_13, da529_3, dm365_3, fa171_1, lp572_2, pe246_1, qf122_3, qv538_1, and ys20_1 were deposited on April 2, 1999 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC
15 207187, from which each clone comprising a particular polynucleotide is obtainable.

Clone as180_1 was deposited on August 11, 1999 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC XXXXXX, from which the as180_1 clone comprising a particular polynucleotide is
20 obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

25 Each clone has been transfected into separate bacterial cells (*E. coli*) in the above composite deposits. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively, or in the case of clone qs14_3,
30 in the pCMVSPORT2 vector (Life Technologies, Inc., Rockville, MD 20850, U.S.A.) depicted in Figure 2. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and

insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for
 5 placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

10 An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

15	<u>Clone</u>	<u>Probe Sequence</u>
	co62_12	SEQ ID NO:161
	lo311_8	SEQ ID NO:162
	ns197_1	SEQ ID NO:163
	pj193_5	SEQ ID NO:164
20	pj317_2	SEQ ID NO:165
	pt332_1	SEQ ID NO:166
	qc297_15	SEQ ID NO:167
	qg596_12	SEQ ID NO:168
	rb649_3	SEQ ID NO:169
25	ca106_19x	SEQ ID NO:170
	ci52_2	SEQ ID NO:171
	md124_16	SEQ ID NO:172
	pk366_7	SEQ ID NO:173
	pl741_5	SEQ ID NO:174
30	pp314_19	SEQ ID NO:175
	pv35_1	SEQ ID NO:176
	pw337_6	SEQ ID NO:177
	rd610_1	SEQ ID NO:178
	rd810_6	SEQ ID NO:179

	cf85_1	SEQ ID NO:180
	dd504_18	SEQ ID NO:181
	np26_3	SEQ ID NO:182
	pm412_12	SEQ ID NO:183
5	pm421_3	SEQ ID NO:184
	pv6_1	SEQ ID NO:185
	qs14_3	SEQ ID NO:186
	qy338_9	SEQ ID NO:187
	rc58_1	SEQ ID NO:188
10	rd232_5	SEQ ID NO:189
	ck213_12	SEQ ID NO:190
	pg195_1	SEQ ID NO:191
	pw460_5	SEQ ID NO:192
	qa136_1	SEQ ID NO:193
15	qy1261_2	SEQ ID NO:194
	rd432_4	SEQ ID NO:195
	rb789_14	SEQ ID NO:196
	yd137_1	SEQ ID NO:197
	ye11_1	SEQ ID NO:198
20	ye72_1	SEQ ID NO:199
	ye78_1	SEQ ID NO:200
	ye90_1	SEQ ID NO:201
	yk251_1	SEQ ID NO:202
	yt14_1	SEQ ID NO:203
25	bf157_16	SEQ ID NO:204
	bk343_2	SEQ ID NO:205
	cd205_2	SEQ ID NO:206
	cw1292_8	SEQ ID NO:207
	cw1475_2	SEQ ID NO:208
30	dd428_4	SEQ ID NO:209
	dh1073_12	SEQ ID NO:210
	dw78_1	SEQ ID NO:211
	fh116_11	SEQ ID NO:212
	fy356_14	SEQ ID NO:213

	iw66_1	SEQ ID NO:214
	kh13_4	SEQ ID NO:215
	ko258_4	SEQ ID NO:216
	kv10_8	SEQ ID NO:217
5	LL89_3	SEQ ID NO:218
	mc300_1	SEQ ID NO:219
	ml227_1	SEQ ID NO:220
	mm367_6	SEQ ID NO:221
	mt124_3	SEQ ID NO:222
10	nf56_3	SEQ ID NO:223
	qy442_2	SEQ ID NO:224
	rj214_14	SEQ ID NO:225
	rk80_3	SEQ ID NO:226
	au36_42	SEQ ID NO:227
15	bo549_13	SEQ ID NO:228
	da529_3	SEQ ID NO:229
	dm365_3	SEQ ID NO:230
	fa171_1	SEQ ID NO:231
	lp572_2	SEQ ID NO:232
20	pe246_1	SEQ ID NO:233
	qf122_3	SEQ ID NO:234
	qv538_1	SEQ ID NO:235
	ys20_1	SEQ ID NO:236
	as180_1	SEQ ID NO:237
25		

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;

- (b) It should be designed to have a T_m of approx. 80 °C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with γ -³²P ATP (specific activity 6000 Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmole.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 µl of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 µg/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 µg/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 µg/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, *Bio/Technology* 10, 773-778 (1992) and in R.S. McDowell, *et al.*, *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that

has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately
5 labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public
10 databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the
polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can
15 then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters"
so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The
desired change in gene expression can be achieved through the use of antisense
20 polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by reference herein). The desired change in gene
expression can also be achieved through the use of double-stranded ribonucleotide
25 molecules having some complementarity to the mRNA transcribed from the gene, and which interfere with the transcription, stability, or expression of the mRNA ("RNA
intereference" or "RNAi"; Fire *et al.*, 1998, *Nature* 391 (6669): 806-811; Montgomery *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* 95 (26): 15502-15507; and Sharp, 1999, *Genes Dev.* 13 (2):
139-141; all of which are incorporated by reference herein). Transgenic animals that have
30 multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are
stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce
gene expression levels, or that change temporal or spatial patterns of gene expression, are

also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through
5 deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination,
10 preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for
15 the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part
20 or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of
25 transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most
30 preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are

proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

5 In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* 266: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of*
10 *Molecular Biology* 215: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* 3: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* 90: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX
15 platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely
20 used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length
25 one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six,
30 seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps.

The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90%

identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and
5 screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly
10 stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [†]	Hybridization Temperature and Buffer [‡]	Wash Temperature and Buffer [‡]
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	<50	T _B *; 1xSSC	T _B *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	<50	T _D *; 1xSSC	T _D *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	RNA:RNA	<50	T _F *; 1xSSC	T _F *; 1xSSC
10	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	<50	T _H *; 4xSSC	T _H *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	<50	T _J *; 4xSSC	T _J *; 4xSSC
	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	<50	T _L *; 2xSSC	T _L *; 2xSSC
15	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	<50	T _N *; 6xSSC	T _N *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	DNA:RNA	<50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	<50	T _R *; 4xSSC	T _R *; 4xSSC

[†] The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

[‡] SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log₁₀[Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds.,

5 John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or
10 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide encoding the protein of the invention may be operably
15 linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined
20 herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the
25 protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

30 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial

strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art

given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

5 The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies
10 or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express
15 recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare
20 with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for
25 examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those
30 described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine
5 levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the
10 protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent
15 grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to
20 Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein
25 or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention
30 can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may

induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is

- 5 evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 10 Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986;
- 15 Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

- Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.
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- Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983;
- 25
- 30 Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;

Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term

tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

- 5 The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as
- 10 described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.
- 15 Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.
- 20 Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from
- 25 the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and
- 30 murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune

response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2

microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated
5 immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated
10 immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without
15 limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al.,
20 J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al.,
25 Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro*
30 antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek,

D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

- 5 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995;
- 10 Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others,
- 15 proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993;
- 20 Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

- Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

25

Hematopoiesis Regulating Activity

- A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell
- 30 lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid

cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and

Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

5

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns,
10 incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as
15 well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal
20 disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue
25 destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in
30 circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The

5 compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal

10 tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and

15 peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's,

20 Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the

25 invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for

30 generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation

of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et al.

APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

5 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting
10 formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

20 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands,
25 receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant
30 receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static
5 conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

10 Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the
15 inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic
20 inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

25

Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to
30 tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved

extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this
5 recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells
10 become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas
15 to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed
20 in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the
25 inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block
30 the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s);

effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic
5 lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another
10 material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a
15 pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the
20 carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other
25 agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor,
30 thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical

compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in
5 combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If
10 administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical
15 composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is
20 administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention.
25 When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid
30 form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present

invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should

5 contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

10 The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician

15 will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100

20 mg (preferably about 0.1mg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is

25 contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain

30 polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein.

Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of
5 antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, *Monoclonal antibodies: principles and practice*, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in *Current Protocols in Immunology*, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the
10 relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, *supra*; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in *Current Protocols in Immunology*, Unit 2.8, Greene Publishing
15 Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be
20 produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* 14: 845-851; Mendez *et al.*, 1997, *Nature Genetics* 15: 146-156 (erratum *Nature Genetics* 16: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide
25 immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, *FEBS Lett.* 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful
30 diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where

abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

5 For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably
10 be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the
15 methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical
20 applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium
25 sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other
30 ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions
5 from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of
10 carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to
15 provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in
20 question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to
25 humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of
30 a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect

the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such
5 polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present
10 invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if
fully set forth.

15

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - (a) the nucleotide sequence of SEQ ID NO:1;
 - 5 (b) the nucleotide sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 821;
 - (c) the nucleotide sequence of SEQ ID NO:1 from nucleotide 120 to nucleotide 821;
 - (d) the nucleotide sequence of SEQ ID NO:1 from nucleotide 1 to
10 nucleotide 1625;
 - (e) the nucleotide sequence of the full-length protein coding sequence of clone co62_12 deposited under accession number ATCC 98825;
 - (f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;
 - 15 (g) the nucleotide sequence of a mature protein coding sequence of clone co62_12 deposited under accession number ATCC 98825;
 - (h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;
 - (i) a nucleotide sequence encoding a protein comprising the amino
20 acid sequence of SEQ ID NO:2;
 - (j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
 - (k) the nucleotide sequence of a polynucleotide that hybridizes under
25 conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and
 - (l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and
30 that has a length that is at least 25% of the length of SEQ ID NO:1.
2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.

3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:
 - (a) growing a culture of a host cell in a suitable culture medium, wherein the host cell has been transformed with the polynucleotide of claim 2; and
 - (b) purifying said protein from the culture.
6. A protein produced according to the process of claim 5.
7. An isolated polynucleotide encoding the protein of claim 6.
8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone co62_12 deposited under accession number ATCC 98825.
9. A protein comprising an amino acid sequence selected from the group consisting of:
 - (a) the amino acid sequence of SEQ ID NO:2;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;
- the protein being substantially free from other mammalian proteins.
10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.
11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.
12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:3;
- (b) the nucleotide sequence of SEQ ID NO:3 from nucleotide 9 to nucleotide 1013;
- (c) the nucleotide sequence of SEQ ID NO:3 from nucleotide 96 to nucleotide 1013;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone lo311_8 deposited under accession number ATCC 98825;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825;
- (f) the nucleotide sequence of a mature protein coding sequence of clone lo311_8 deposited under accession number ATCC 98825;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:3.

13. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
- (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and
- (c) the amino acid sequence encoded by the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825;
- the protein being substantially free from other mammalian proteins.

14. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:5;
- 5 (b) the nucleotide sequence of SEQ ID NO:5 from nucleotide 352 to nucleotide 825;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ns197_1 deposited under accession number ATCC 98825;
- (d) a nucleotide sequence encoding the full-length protein encoded by
10 the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (f) a nucleotide sequence encoding a protein comprising a fragment
15 of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under
20 conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:5.

15. A protein comprising an amino acid sequence selected from the group
25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
30 ns197_1 deposited under accession number ATCC 98825;
- the protein being substantially free from other mammalian proteins.

16. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:7;
- (b) the nucleotide sequence of SEQ ID NO:7 from nucleotide 86 to nucleotide 829;
- (c) the nucleotide sequence of SEQ ID NO:7 from nucleotide 149 to nucleotide 829;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone pj193_5 deposited under accession number ATCC 98825;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pj193_5 deposited under accession number ATCC 98825;
- (f) the nucleotide sequence of a mature protein coding sequence of clone pj193_5 deposited under accession number ATCC 98825;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pj193_5 deposited under accession number ATCC 98825;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:7.

17. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
- (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pj193_5 deposited under accession number ATCC 98825;
- the protein being substantially free from other mammalian proteins.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:9;
- 5 (b) the nucleotide sequence of SEQ ID NO:9 from nucleotide 174 to nucleotide 1292;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pj317_2 deposited under accession number ATCC 98825;
- (d) a nucleotide sequence encoding the full-length protein encoded by
10 the cDNA insert of clone pj317_2 deposited under accession number ATCC 98825;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (f) a nucleotide sequence encoding a protein comprising a fragment
15 of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 20 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:9.

19. A protein comprising an amino acid sequence selected from the group
25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
30 pj317_2 deposited under accession number ATCC 98825;
- the protein being substantially free from other mammalian proteins.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:11;
- (b) the nucleotide sequence of SEQ ID NO:11 from nucleotide 7 to nucleotide 2517;
- (c) the nucleotide sequence of SEQ ID NO:11 from nucleotide 904 to nucleotide 2517;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone pt332_1 deposited under accession number ATCC 98825;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;
- (f) the nucleotide sequence of a mature protein coding sequence of clone pt332_1 deposited under accession number ATCC 98825;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:11.

21. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
- (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;
- the protein being substantially free from other mammalian proteins.

22. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:13;
- 5 (b) the nucleotide sequence of SEQ ID NO:13 from nucleotide 18 to nucleotide 257;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone qc297_15 deposited under accession number ATCC 98825;
- 10 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- 15 (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 20 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:13.

25 23. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
 - 30 (c) the amino acid sequence encoded by the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825;
- the protein being substantially free from other mammalian proteins.

24. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:15;
- (b) the nucleotide sequence of SEQ ID NO:15 from nucleotide 21 to
5 nucleotide 2432;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone qg596_12 deposited under accession number ATCC 98825;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qg596_12 deposited under accession number ATCC
10 98825;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight
15 contiguous amino acids of SEQ ID NO:16;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under
20 conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:15.

25. A protein comprising an amino acid sequence selected from the group
25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
30 qg596_12 deposited under accession number ATCC 98825;
- the protein being substantially free from other mammalian proteins.

26. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:17;
- (b) the nucleotide sequence of SEQ ID NO:17 from nucleotide 339 to nucleotide 2105;
- (c) the nucleotide sequence of SEQ ID NO:17 from nucleotide 501 to nucleotide 2105;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone rb649_3 deposited under accession number ATCC 98825;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;
- (f) the nucleotide sequence of a mature protein coding sequence of clone rb649_3 deposited under accession number ATCC 98825;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:17.

27. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and
- (c) the amino acid sequence encoded by the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;
- the protein being substantially free from other mammalian proteins.

28. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:19;
- 5 (b) the nucleotide sequence of SEQ ID NO:19 from nucleotide 509 to nucleotide 2467;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ca106_19x deposited under accession number ATCC 98835;
- (d) a nucleotide sequence encoding the full-length protein encoded by
10 the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (f) a nucleotide sequence encoding a protein comprising a fragment
15 of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 20 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:19.

25 29. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:20, the
fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
 - 30 (c) the amino acid sequence encoded by the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;
- the protein being substantially free from other mammalian proteins.

30. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:21;
- (b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 179 to
5 nucleotide 802;
- (c) the nucleotide sequence of SEQ ID NO:21 from nucleotide 242 to
nucleotide 802;
- (d) the nucleotide sequence of the full-length protein coding sequence
of clone ci52_2 deposited under accession number ATCC 98835;
- 10 (e) a nucleotide sequence encoding the full-length protein encoded by
the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835;
- (f) the nucleotide sequence of a mature protein coding sequence of
clone ci52_2 deposited under accession number ATCC 98835;
- (g) a nucleotide sequence encoding a mature protein encoded by the
15 cDNA insert of clone ci52_2 deposited under accession number ATCC 98835;
- (h) a nucleotide sequence encoding a protein comprising the amino
acid sequence of SEQ ID NO:22;
- (i) a nucleotide sequence encoding a protein comprising a fragment
of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight
20 contiguous amino acids of SEQ ID NO:22;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees
C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- 25 (k) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees
C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and
that has a length that is at least 25% of the length of SEQ ID NO:21.

31. A protein comprising an amino acid sequence selected from the group
30 consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
- (b) a fragment of the amino acid sequence of SEQ ID NO:22, the
fragment comprising eight contiguous amino acids of SEQ ID NO:22; and

(c) the amino acid sequence encoded by the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835; the protein being substantially free from other mammalian proteins.

- 5 32. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:23;
 - (b) the nucleotide sequence of SEQ ID NO:23 from nucleotide 46 to nucleotide 714;
 - 10 (c) the nucleotide sequence of SEQ ID NO:23 from nucleotide 538 to nucleotide 714;
 - (d) the nucleotide sequence of the full-length protein coding sequence of clone md124_16 deposited under accession number ATCC 98835;
 - (e) a nucleotide sequence encoding the full-length protein encoded by
15 the cDNA insert of clone md124_16 deposited under accession number ATCC 98835;
 - (f) the nucleotide sequence of a mature protein coding sequence of clone md124_16 deposited under accession number ATCC 98835;
 - (g) a nucleotide sequence encoding a mature protein encoded by the
20 cDNA insert of clone md124_16 deposited under accession number ATCC 98835;
 - (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:24;
 - (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight
25 contiguous amino acids of SEQ ID NO:24;
 - (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
 - (k) the nucleotide sequence of a polynucleotide that hybridizes under
30 conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:23.

33. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:24;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:24, the
5 fragment comprising eight contiguous amino acids of SEQ ID NO:24; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
md124_16 deposited under accession number ATCC 98835;
- the protein being substantially free from other mammalian proteins.

10 34. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:25;
- (b) the nucleotide sequence of SEQ ID NO:25 from nucleotide 92 to
nucleotide 1726;
- 15 (c) the nucleotide sequence of SEQ ID NO:25 from nucleotide 1211 to
nucleotide 1726;
- (d) the nucleotide sequence of the full-length protein coding sequence
of clone pk366_7 deposited under accession number ATCC 98835;
- (e) a nucleotide sequence encoding the full-length protein encoded by
20 the cDNA insert of clone pk366_7 deposited under accession number ATCC 98835;
- (f) the nucleotide sequence of a mature protein coding sequence of
clone pk366_7 deposited under accession number ATCC 98835;
- (g) a nucleotide sequence encoding a mature protein encoded by the
cDNA insert of clone pk366_7 deposited under accession number ATCC 98835;
- 25 (h) a nucleotide sequence encoding a protein comprising the amino
acid sequence of SEQ ID NO:26;
- (i) a nucleotide sequence encoding a protein comprising a fragment
of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight
contiguous amino acids of SEQ ID NO:26;
- 30 (j) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees
C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:25.

35. A protein comprising an amino acid sequence selected from the group
5 consisting of:
- (a) the amino acid sequence of SEQ ID NO:26;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 pk366_7 deposited under accession number ATCC 98835;
- the protein being substantially free from other mammalian proteins.
36. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- 15 (a) the nucleotide sequence of SEQ ID NO:27;
 - (b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 16 to nucleotide 1788;
 - (c) the nucleotide sequence of SEQ ID NO:27 from nucleotide 61 to nucleotide 1788;
 - 20 (d) the nucleotide sequence of the full-length protein coding sequence of clone pl741_5 deposited under accession number ATCC 98835;
 - (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;
 - (f) the nucleotide sequence of a mature protein coding sequence of
25 clone pl741_5 deposited under accession number ATCC 98835;
 - (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;
 - (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
 - 30 (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:27.

37. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
- (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;
- the protein being substantially free from other mammalian proteins.

38. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:29;
- (b) the nucleotide sequence of SEQ ID NO:29 from nucleotide 629 to nucleotide 2338;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pp314_19 deposited under accession number ATCC 98835;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 5 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:29.

39. A protein comprising an amino acid sequence selected from the group
- 10 consisting of:
- (a) the amino acid sequence of SEQ ID NO:30;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
- 15 pp314_19 deposited under accession number ATCC 98835;
- the protein being substantially free from other mammalian proteins.

40. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- 20 (a) the nucleotide sequence of SEQ ID NO:31;
- (b) the nucleotide sequence of SEQ ID NO:31 from nucleotide 158 to nucleotide 1102;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pv35_1 deposited under accession number ATCC 98835;
- 25 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:32;
- (f) a nucleotide sequence encoding a protein comprising a fragment
- 30 of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:31.

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41. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:32, the
10 fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
pv35_1 deposited under accession number ATCC 98835;
- the protein being substantially free from other mammalian proteins.

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42. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:33;
- (b) the nucleotide sequence of SEQ ID NO:33 from nucleotide 413 to
nucleotide 733;
- (c) the nucleotide sequence of the full-length protein coding sequence
20 of clone pw337_6 deposited under accession number ATCC 98835;
- (d) a nucleotide sequence encoding the full-length protein encoded by
the cDNA insert of clone pw337_6 deposited under accession number ATCC
98835;
- (e) a nucleotide sequence encoding a protein comprising the amino
25 acid sequence of SEQ ID NO:34;
- (f) a nucleotide sequence encoding a protein comprising a fragment
of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight
contiguous amino acids of SEQ ID NO:34;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under
30 conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees
C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:33.

43. A protein comprising an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 pw337_6 deposited under accession number ATCC 98835;
- the protein being substantially free from other mammalian proteins.

44. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- 15 (a) the nucleotide sequence of SEQ ID NO:35;
- (b) the nucleotide sequence of SEQ ID NO:35 from nucleotide 678 to nucleotide 938;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone rd610_1 deposited under accession number ATCC 98835;
- 20 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (f) a nucleotide sequence encoding a protein comprising a fragment
25 of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 30 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:35.

45. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:36, the
5 fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
rd610_1 deposited under accession number ATCC 98835;
- the protein being substantially free from other mammalian proteins.

10 46. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO.;
- (b) the nucleotide sequence of SEQ ID NO: from nucleotide 75 to
nucleotide 494;
- 15 (c) the nucleotide sequence of SEQ ID NO: from nucleotide 447 to
nucleotide 494;
- (d) the nucleotide sequence of the full-length protein coding sequence
of clone rd810_6 deposited under accession number ATCC 98835;
- (e) a nucleotide sequence encoding the full-length protein encoded by
20 the cDNA insert of clone rd810_6 deposited under accession number ATCC 98835;
- (f) the nucleotide sequence of a mature protein coding sequence of
clone rd810_6 deposited under accession number ATCC 98835;
- (g) a nucleotide sequence encoding a mature protein encoded by the
cDNA insert of clone rd810_6 deposited under accession number ATCC 98835;
- 25 (h) a nucleotide sequence encoding a protein comprising the amino
acid sequence of SEQ ID NO.;
- (i) a nucleotide sequence encoding a protein comprising a fragment
of the amino acid sequence of SEQ ID NO., the fragment comprising eight
contiguous amino acids of SEQ ID NO.;
- 30 (j) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees
C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:.

47. A protein comprising an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:;
- (b) a fragment of the amino acid sequence of SEQ ID NO:; the fragment comprising eight contiguous amino acids of SEQ ID NO:; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
10 rd810_6 deposited under accession number ATCC 98835;
the protein being substantially free from other mammalian proteins.

48. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- 15 (a) the nucleotide sequence of SEQ ID NO:39;
- (b) the nucleotide sequence of SEQ ID NO:39 from nucleotide 181 to nucleotide 1080;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone cf85_1 deposited under accession number ATCC 98850;
- 20 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- (f) a nucleotide sequence encoding a protein comprising a fragment
25 of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 30 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:39.

49. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850;
- the protein being substantially free from other mammalian proteins.

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50. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:41;
- (b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 161 to
- 15 nucleotide 1348;
- (c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 599 to nucleotide 1348;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone dd504_18 deposited under accession number ATCC 98850;
- 20 (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;
- (f) the nucleotide sequence of a mature protein coding sequence of clone dd504_18 deposited under accession number ATCC 98850;
- 25 (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (i) a nucleotide sequence encoding a protein comprising a fragment
- 30 of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:41.

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51. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:42, the
10 fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;
- the protein being substantially free from other mammalian proteins.

15

52. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:43;
- (b) the nucleotide sequence of SEQ ID NO:43 from nucleotide 70 to
nucleotide 1386;
- (c) the nucleotide sequence of the full-length protein coding sequence
20 of clone np26_3 deposited under accession number ATCC 98850;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone np26_3 deposited under accession number ATCC 98850;
- (e) a nucleotide sequence encoding a protein comprising the amino
25 acid sequence of SEQ ID NO:44;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under
30 conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:43.

53. A protein comprising an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:44;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 np26_3 deposited under accession number ATCC 98850;
- the protein being substantially free from other mammalian proteins.

54. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- 15 (a) the nucleotide sequence of SEQ ID NO:45;
- (b) the nucleotide sequence of SEQ ID NO:45 from nucleotide 60 to nucleotide 3515;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pm412_12 deposited under accession number ATCC 98850;
- 20 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- 25 (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 30 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:45.

55. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:46, the
5 fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;
- the protein being substantially free from other mammalian proteins.

10 56. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:47;
- (b) the nucleotide sequence of SEQ ID NO:47 from nucleotide 1490 to
nucleotide 1780;
- 15 (c) the nucleotide sequence of SEQ ID NO:47 from nucleotide 1556 to
nucleotide 1780;
- (d) the nucleotide sequence of the full-length protein coding sequence
of clone pm421_3 deposited under accession number ATCC 98850;
- (e) a nucleotide sequence encoding the full-length protein encoded by
20 the cDNA insert of clone pm421_3 deposited under accession number ATCC
98850;
- (f) the nucleotide sequence of a mature protein coding sequence of
clone pm421_3 deposited under accession number ATCC 98850;
- (g) a nucleotide sequence encoding a mature protein encoded by the
25 cDNA insert of clone pm421_3 deposited under accession number ATCC 98850;
- (h) a nucleotide sequence encoding a protein comprising the amino
acid sequence of SEQ ID NO:48;
- (i) a nucleotide sequence encoding a protein comprising a fragment
of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight
30 contiguous amino acids of SEQ ID NO:48;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees
C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:47.

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57. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:48, the
10 fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
pm421_3 deposited under accession number ATCC 98850;
- the protein being substantially free from other mammalian proteins.

15 58. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:49;
- (b) the nucleotide sequence of SEQ ID NO:49 from nucleotide 64 to
nucleotide 486;
- 20 (c) the nucleotide sequence of SEQ ID NO:49 from nucleotide 217 to
nucleotide 486;
- (d) the nucleotide sequence of the full-length protein coding sequence
of clone pv6_1 deposited under accession number ATCC 98850;
- (e) a nucleotide sequence encoding the full-length protein encoded by
25 the cDNA insert of clone pv6_1 deposited under accession number ATCC 98850;
- (f) the nucleotide sequence of a mature protein coding sequence of
clone pv6_1 deposited under accession number ATCC 98850;
- (g) a nucleotide sequence encoding a mature protein encoded by the
cDNA insert of clone pv6_1 deposited under accession number ATCC 98850;
- 30 (h) a nucleotide sequence encoding a protein comprising the amino
acid sequence of SEQ ID NO:50;
- (i) a nucleotide sequence encoding a protein comprising a fragment
of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight
contiguous amino acids of SEQ ID NO:50;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:49.

59. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:50;
- (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pv6_1 deposited under accession number ATCC 98850;
- the protein being substantially free from other mammalian proteins.

60. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:51;
- (b) the nucleotide sequence of SEQ ID NO:51 from nucleotide 379 to nucleotide 3783;
- (c) the nucleotide sequence of SEQ ID NO:51 from nucleotide 460 to nucleotide 3783;
- (d) the nucleotide sequence of SEQ ID NO:51 from nucleotide 1983 to nucleotide 3938;
- (e) the nucleotide sequence of the full-length protein coding sequence of clone qs14_3 deposited under accession number ATCC 98850;
- (f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850;
- (g) the nucleotide sequence of a mature protein coding sequence of clone qs14_3 deposited under accession number ATCC 98850;
- (h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850;

- (i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and
- (l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:51.
61. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:52;
- (b) the amino acid sequence of SEQ ID NO:52 from amino acid 536 to amino acid 1135;
- (c) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
- (d) the amino acid sequence encoded by the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850;
- the protein being substantially free from other mammalian proteins.
62. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:53;
- (b) the nucleotide sequence of SEQ ID NO:53 from nucleotide 1 to nucleotide 843;
- (c) the nucleotide sequence of SEQ ID NO:53 from nucleotide 469 to nucleotide 843;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone qy338_9 deposited under accession number ATCC 98850;

- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qy338_9 deposited under accession number ATCC 98850;
- (f) the nucleotide sequence of a mature protein coding sequence of clone qy338_9 deposited under accession number ATCC 98850;
- 5 (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone qy338_9 deposited under accession number ATCC 98850;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:54;
- 10 (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- 15 (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:53.
- 20 63. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:54;
- (b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone qy338_9 deposited under accession number ATCC 98850;
- the protein being substantially free from other mammalian proteins.
64. An isolated polynucleotide comprising a nucleotide sequence selected from
- 30 the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:55;
- (b) the nucleotide sequence of SEQ ID NO:55 from nucleotide 283 to nucleotide 906;

- (c) the nucleotide sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 906;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone rc58_1 deposited under accession number ATCC 98850;
- 5 (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;
- (f) the nucleotide sequence of a mature protein coding sequence of clone rc58_1 deposited under accession number ATCC 98850;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;
- 10 (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- 15 (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:55.
- 20
65. A protein comprising an amino acid sequence selected from the group consisting of:
- 25 (a) the amino acid sequence of SEQ ID NO:56;
- (b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
- (c) the amino acid sequence encoded by the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;
- 30 the protein being substantially free from other mammalian proteins.

66. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:57;
- (b) the nucleotide sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 973;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone rd232_5 deposited under accession number ATCC 98850;
- 5 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- 10 (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 15 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:57.
- 20
67. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:58;
- (b) a fragment of the amino acid sequence of SEQ ID NO:58, the
- 25 fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
- (c) the amino acid sequence encoded by the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850;
- the protein being substantially free from other mammalian proteins.
- 30
68. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:59;
- (b) the nucleotide sequence of SEQ ID NO:59 from nucleotide 893 to nucleotide 2596;

- (c) the nucleotide sequence of the full-length protein coding sequence of clone ck213_12 deposited under accession number ATCC 98918;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:59.

69. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:60;
- (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;
- the protein being substantially free from other mammalian proteins.

70. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:61;
- (b) the nucleotide sequence of SEQ ID NO:61 from nucleotide 29 to nucleotide 1750;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pg195_1 deposited under accession number ATCC 98918;

- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:62;
- 5 (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 10 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:61.
- 15
71. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:62;
- (b) a fragment of the amino acid sequence of SEQ ID NO:62, the
- 20 fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918;
- the protein being substantially free from other mammalian proteins.
- 25
72. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:63;
- (b) the nucleotide sequence of SEQ ID NO:63 from nucleotide 1147 to nucleotide 1440;
- 30 (c) the nucleotide sequence of SEQ ID NO:63 from nucleotide 1234 to nucleotide 1440;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone pw460_5 deposited under accession number ATCC 98918;

- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918;
- (f) the nucleotide sequence of a mature protein coding sequence of clone pw460_5 deposited under accession number ATCC 98918;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:64;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:63.
73. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:64;
- (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918;
- the protein being substantially free from other mammalian proteins.
74. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:65;
- (b) the nucleotide sequence of SEQ ID NO:65 from nucleotide 46 to nucleotide 1356;

- (c) the nucleotide sequence of SEQ ID NO:65 from nucleotide 127 to nucleotide 1356;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone qa136_1 deposited under accession number ATCC 98918;
- 5 (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;
- (f) the nucleotide sequence of a mature protein coding sequence of clone qa136_1 deposited under accession number ATCC 98918;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;
- 10 (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- 15 (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:65.
- 20

75. A protein comprising an amino acid sequence selected from the group consisting of:

25

- (a) the amino acid sequence of SEQ ID NO:66;
- (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;
- 30 the protein being substantially free from other mammalian proteins.

76. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:67;
- (b) the nucleotide sequence of SEQ ID NO:67 from nucleotide 206 to nucleotide 1624;
- (c) the nucleotide sequence of SEQ ID NO:67 from nucleotide 542 to nucleotide 1624;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone qy1261_2 deposited under accession number ATCC 98918;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918;
- (f) the nucleotide sequence of a mature protein coding sequence of clone qy1261_2 deposited under accession number ATCC 98918;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:67.

77. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
- (b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918;

the protein being substantially free from other mammalian proteins.

78. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- 5 (a) the nucleotide sequence of SEQ ID NO:69;
- (b) the nucleotide sequence of SEQ ID NO:69 from nucleotide 1359 to nucleotide 1817;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone rd432_4 deposited under accession number ATCC 98918;
- 10 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:70;
- (f) a nucleotide sequence encoding a protein comprising a fragment
15 of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 20 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:69.

25 79. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:70;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:70, the
fragment comprising eight contiguous amino acids of SEQ ID NO:70; and
 - 30 (c) the amino acid sequence encoded by the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918;
- the protein being substantially free from other mammalian proteins.

80. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:71;
- (b) the nucleotide sequence of SEQ ID NO:71 from nucleotide 884 to
5 nucleotide 1195;
- (c) the nucleotide sequence of SEQ ID NO:71 from nucleotide 947 to
nucleotide 1195;
- (d) the nucleotide sequence of the full-length protein coding sequence
of clone rb789_14 deposited under accession number ATCC 207004;
- 10 (e) a nucleotide sequence encoding the full-length protein encoded by
the cDNA insert of clone rb789_14 deposited under accession number ATCC
207004;
- (f) the nucleotide sequence of a mature protein coding sequence of
clone rb789_14 deposited under accession number ATCC 207004;
- 15 (g) a nucleotide sequence encoding a mature protein encoded by the
cDNA insert of clone rb789_14 deposited under accession number ATCC 207004;
- (h) a nucleotide sequence encoding a protein comprising the amino
acid sequence of SEQ ID NO:72;
- (i) a nucleotide sequence encoding a protein comprising a fragment
20 of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight
contiguous amino acids of SEQ ID NO:72;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees
C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- 25 (k) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees
C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and
that has a length that is at least 25% of the length of SEQ ID NO:71.

30 81. A protein comprising an amino acid sequence selected from the group
consisting of:

- (a) the amino acid sequence of SEQ ID NO:72;
- (b) a fragment of the amino acid sequence of SEQ ID NO:72, the
fragment comprising eight contiguous amino acids of SEQ ID NO:72; and

(c) the amino acid sequence encoded by the cDNA insert of clone rb789_14 deposited under accession number ATCC 207004; the protein being substantially free from other mammalian proteins.

- 5 82. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:73;
 - (b) the nucleotide sequence of SEQ ID NO:73 from nucleotide 69 to nucleotide 374;
 - 10 (c) the nucleotide sequence of SEQ ID NO:73 from nucleotide 186 to nucleotide 374;
 - (d) the nucleotide sequence of the full-length protein coding sequence of clone yd137_1 deposited under accession number ATCC 207004;
 - (e) a nucleotide sequence encoding the full-length protein encoded by
15 the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;
 - (f) the nucleotide sequence of a mature protein coding sequence of clone yd137_1 deposited under accession number ATCC 207004;
 - (g) a nucleotide sequence encoding a mature protein encoded by the
20 cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;
 - (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:74;
 - (i) a nucleotide sequence encoding a protein comprising a fragment
25 of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;
 - (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
 - (k) the nucleotide sequence of a polynucleotide that hybridizes under
30 conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:73.

83. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:74, the
5 fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;
- the protein being substantially free from other mammalian proteins.

10 84. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:75;
- (b) the nucleotide sequence of SEQ ID NO:75 from nucleotide 8 to
nucleotide 343;
- 15 (c) the nucleotide sequence of SEQ ID NO:75 from nucleotide 50 to
nucleotide 343;
- (d) the nucleotide sequence of the full-length protein coding sequence
of clone yd218_1 deposited under accession number ATCC 207004;
- (e) a nucleotide sequence encoding the full-length protein encoded by
20 the cDNA insert of clone yd218_1 deposited under accession number ATCC
207004;
- (f) the nucleotide sequence of a mature protein coding sequence of
clone yd218_1 deposited under accession number ATCC 207004;
- (g) a nucleotide sequence encoding a mature protein encoded by the
25 cDNA insert of clone yd218_1 deposited under accession number ATCC 207004;
- (h) a nucleotide sequence encoding a protein comprising the amino
acid sequence of SEQ ID NO:76;
- (i) a nucleotide sequence encoding a protein comprising a fragment
of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight
30 contiguous amino acids of SEQ ID NO:76;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees
C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:75.

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85. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:76, the
10 fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004;
- the protein being substantially free from other mammalian proteins.

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86. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:77;
- (b) the nucleotide sequence of SEQ ID NO:77 from nucleotide 84 to
nucleotide 1679;
- (c) the nucleotide sequence of the full-length protein coding sequence
20 of clone ye11_1 deposited under accession number ATCC 207004;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ye11_1 deposited under accession number ATCC 207004;
- (e) a nucleotide sequence encoding a protein comprising the amino
25 acid sequence of SEQ ID NO:78;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under
30 conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:77.

87. A protein comprising an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- (b) a fragment of the amino acid sequence of SEQ ID NO:78, the
fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
10 ye11_1 deposited under accession number ATCC 207004;
the protein being substantially free from other mammalian proteins.

88. An isolated polynucleotide comprising a nucleotide sequence selected from
the group consisting of:

- 15 (a) the nucleotide sequence of SEQ ID NO:79;
- (b) the nucleotide sequence of SEQ ID NO:79 from nucleotide 72 to
nucleotide 1646;
- (c) the nucleotide sequence of SEQ ID NO:79 from nucleotide 180 to
nucleotide 1646;
- 20 (d) the nucleotide sequence of the full-length protein coding sequence
of clone ye72_1 deposited under accession number ATCC 207004;
- (e) a nucleotide sequence encoding the full-length protein encoded by
the cDNA insert of clone ye72_1 deposited under accession number ATCC 207004;
- (f) the nucleotide sequence of a mature protein coding sequence of
25 clone ye72_1 deposited under accession number ATCC 207004;
- (g) a nucleotide sequence encoding a mature protein encoded by the
cDNA insert of clone ye72_1 deposited under accession number ATCC 207004;
- (h) a nucleotide sequence encoding a protein comprising the amino
acid sequence of SEQ ID NO:80;
- 30 (i) a nucleotide sequence encoding a protein comprising a fragment
of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight
contiguous amino acids of SEQ ID NO:80;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- 5 (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:79.

89. A protein comprising an amino acid sequence selected from the group
- 10 consisting of:
- (a) the amino acid sequence of SEQ ID NO:80;
- (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
- 15 ye72_1 deposited under accession number ATCC 207004;
- the protein being substantially free from other mammalian proteins.

90. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- 20 (a) the nucleotide sequence of SEQ ID NO:81;
- (b) the nucleotide sequence of SEQ ID NO:81 from nucleotide 954 to nucleotide 2423;
- (c) the nucleotide sequence of SEQ ID NO:81 from nucleotide 1224 to nucleotide 2423;
- 25 (d) the nucleotide sequence of the full-length protein coding sequence of clone ye78_1 deposited under accession number ATCC 207004;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;
- (f) the nucleotide sequence of a mature protein coding sequence of
- 30 clone ye78_1 deposited under accession number ATCC 207004;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:82;

- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;
- 5 (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- 10 (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:81.

91. A protein comprising an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:82;
- (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;
- the protein being substantially free from other mammalian proteins.

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92. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:83;
- 25 (b) the nucleotide sequence of SEQ ID NO:83 from nucleotide 176 to nucleotide 1321;
- (c) the nucleotide sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1321;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ye90_1 deposited under accession number ATCC 207004;
- 30 (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ye90_1 deposited under accession number ATCC 207004;

- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:84;
- 5 (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- 10 (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:83.
- 15
93. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:84;
- (b) a fragment of the amino acid sequence of SEQ ID NO:84, the
- 20 fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;
- the protein being substantially free from other mammalian proteins.
- 25
94. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:85;
- (b) the nucleotide sequence of SEQ ID NO:85 from nucleotide 105 to nucleotide 605;
- 30 (c) the nucleotide sequence of the full-length protein coding sequence of clone yi62_1 deposited under accession number ATCC 207004;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004;

- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:86;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:85.

95. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:86;
- (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004;
- the protein being substantially free from other mammalian proteins.

96. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:87;
- (b) the nucleotide sequence of SEQ ID NO:87 from nucleotide 223 to nucleotide 798;
- (c) the nucleotide sequence of SEQ ID NO:87 from nucleotide 430 to nucleotide 798;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk78_1 deposited under accession number ATCC 207004;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;

- (f) the nucleotide sequence of a mature protein coding sequence of clone yk78_1 deposited under accession number ATCC 207004;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;
- 5 (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- 10 (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and
- 15 that has a length that is at least 25% of the length of SEQ ID NO:87.

97. A protein comprising an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:88;
- (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;
- 25 the protein being substantially free from other mammalian proteins.

98. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:89;
- 30 (b) the nucleotide sequence of SEQ ID NO:89 from nucleotide 211 to nucleotide 942;
- (c) the nucleotide sequence of SEQ ID NO:89 from nucleotide 298 to nucleotide 942;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk251_1 deposited under accession number ATCC 207004;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yk251_1 deposited under accession number ATCC 207004;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:90;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:89.
99. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:90;
- (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;
- the protein being substantially free from other mammalian proteins.

100. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:91;

- (b) the nucleotide sequence of SEQ ID NO:91 from nucleotide 149 to nucleotide 784;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yt14_1 deposited under accession number ATCC 207004;
- 5 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:92;
- (f) a nucleotide sequence encoding a protein comprising a fragment
10 of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 15 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:91.
- 20 101. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:92;
- (b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;
- the protein being substantially free from other mammalian proteins.
102. An isolated polynucleotide comprising a nucleotide sequence selected from
30 the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:93;
- (b) the nucleotide sequence of SEQ ID NO:93 from nucleotide 89 to nucleotide 1441;

- (c) the nucleotide sequence of the full-length protein coding sequence of clone bf157_16 deposited under accession number ATCC 207088;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:94;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:93.

103. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
- (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
- (c) the amino acid sequence encoded by the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088;
- the protein being substantially free from other mammalian proteins.

104. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:95;
- (b) the nucleotide sequence of SEQ ID NO:95 from nucleotide 219 to nucleotide 629;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone bk343_2 deposited under accession number ATCC 207088;

- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088;
- 5 (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:96;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;
- 10 (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and
- 15 that has a length that is at least 25% of the length of SEQ ID NO:95.

105. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:96;
- 20 (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
- (c) the amino acid sequence encoded by the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088;
- the protein being substantially free from other mammalian proteins.

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106. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:97;
- (b) the nucleotide sequence of SEQ ID NO:97 from nucleotide 556 to
- 30 nucleotide 951;
- (c) the nucleotide sequence of SEQ ID NO:97 from nucleotide 868 to nucleotide 951;
- (d) the nucleotide sequence of SEQ ID NO:97 from nucleotide 9 to nucleotide 1295;

- (e) the nucleotide sequence of the full-length protein coding sequence of clone cd205_2 deposited under accession number ATCC 207088;
- (f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088;
- (g) the nucleotide sequence of a mature protein coding sequence of clone cd205_2 deposited under accession number ATCC 207088;
- (h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088;
- (i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
- (j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and
- (l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:97.
107. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:98;
- (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088;
- the protein being substantially free from other mammalian proteins.

108. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:99;

- (b) the nucleotide sequence of SEQ ID NO:99 from nucleotide 216 to nucleotide 443;
- (c) the nucleotide sequence of SEQ ID NO:99 from nucleotide 306 to nucleotide 443;
- 5 (d) the nucleotide sequence of the full-length protein coding sequence of clone cw1292_8 deposited under accession number ATCC 207088;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;
- 10 (f) the nucleotide sequence of a mature protein coding sequence of clone cw1292_8 deposited under accession number ATCC 207088;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- 15 (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- 20 (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and
- 25 that has a length that is at least 25% of the length of SEQ ID NO:99.

109. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
- 30 (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;
- the protein being substantially free from other mammalian proteins.

110. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:101;
- 5 (b) the nucleotide sequence of SEQ ID NO:101 from nucleotide 2136 to nucleotide 2447;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone cw1475_2 deposited under accession number ATCC 207088;
- (d) a nucleotide sequence encoding the full-length protein encoded by
10 the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (f) a nucleotide sequence encoding a protein comprising a fragment
15 of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 20 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:101.

25 111. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:102, the
fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
 - 30 (c) the amino acid sequence encoded by the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088;
- the protein being substantially free from other mammalian proteins.

112. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:103;
- (b) the nucleotide sequence of SEQ ID NO:103 from nucleotide 310 to
5 nucleotide 954;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone dd428_4 deposited under accession number ATCC 207088;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dd428_4 deposited under accession number ATCC
10 207088;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:104;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight
15 contiguous amino acids of SEQ ID NO:104;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under
20 conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:103.

113. A protein comprising an amino acid sequence selected from the group
25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
30 dd428_4 deposited under accession number ATCC 207088;
- the protein being substantially free from other mammalian proteins.

114. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:105;
- (b) the nucleotide sequence of SEQ ID NO:105 from nucleotide 1698 to nucleotide 1895;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone dh1073_12 deposited under accession number ATCC 207088;
- 5 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:106;
- 10 (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 15 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:105.
- 20

115. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:106;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;
- the protein being substantially free from other mammalian proteins.
- 30

116. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:107;

- (b) the nucleotide sequence of SEQ ID NO:107 from nucleotide 423 to nucleotide 791;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone dw78_1 deposited under accession number ATCC 207088;
- 5 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:108;
- 10 (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 15 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:107.
- 20
117. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:108;
- (b) a fragment of the amino acid sequence of SEQ ID NO:108, the
- 25 fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;
- the protein being substantially free from other mammalian proteins.
- 30
118. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:109;
- (b) the nucleotide sequence of SEQ ID NO:109 from nucleotide 96 to nucleotide 944;

- (c) the nucleotide sequence of the full-length protein coding sequence of clone fh116_11 deposited under accession number ATCC 207088;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:110;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:109.

119. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:110;
- (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and
- (c) the amino acid sequence encoded by the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;
- the protein being substantially free from other mammalian proteins.

120. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:111;
- (b) the nucleotide sequence of SEQ ID NO:111 from nucleotide 150 to nucleotide 1610;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone fy356_14 deposited under accession number ATCC 207088;

- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088;
- 5 (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:112;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;
- 10 (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and
- 15 that has a length that is at least 25% of the length of SEQ ID NO:111.

121. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
- 20 (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
- (c) the amino acid sequence encoded by the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088;
- the protein being substantially free from other mammalian proteins.

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122. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:113;
- (b) the nucleotide sequence of SEQ ID NO:113 from nucleotide 49 to
- 30 nucleotide 669;
- (c) the nucleotide sequence of SEQ ID NO:113 from nucleotide 112 to nucleotide 669;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone iw66_1 deposited under accession number ATCC 207088;

- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;
- (f) the nucleotide sequence of a mature protein coding sequence of clone iw66_1 deposited under accession number ATCC 207088;
- 5 (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:114;
- 10 (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- 15 (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:113.
- 20 123. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:114;
- (b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;
- the protein being substantially free from other mammalian proteins.
124. An isolated polynucleotide comprising a nucleotide sequence selected from
- 30 the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:115;
- (b) the nucleotide sequence of SEQ ID NO:115 from nucleotide 165 to nucleotide 416;

- (c) the nucleotide sequence of the full-length protein coding sequence of clone kh13_4 deposited under accession number ATCC 207089;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089;
- 5 (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:116;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;
- 10 (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and
- 15 that has a length that is at least 25% of the length of SEQ ID NO:115.

125. A protein comprising an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:116;
- (b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and
- (c) the amino acid sequence encoded by the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089;
- 25 the protein being substantially free from other mammalian proteins.

126. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:117;
- 30 (b) the nucleotide sequence of SEQ ID NO:117 from nucleotide 204 to nucleotide 602;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ko258_4 deposited under accession number ATCC 207089;

- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089;
- 5 (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:118;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;
- 10 (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and
- 15 that has a length that is at least 25% of the length of SEQ ID NO:117.

127. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:118;
- 20 (b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089;
- the protein being substantially free from other mammalian proteins.

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128. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:119;
- (b) the nucleotide sequence of SEQ ID NO:119 from nucleotide 434 to
- 30 nucleotide 739;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone kv10_8 deposited under accession number ATCC 207089;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089;

- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:120;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120, the fragment comprising eight contiguous amino acids of SEQ ID NO:120;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:119.

129. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:120;
- (b) a fragment of the amino acid sequence of SEQ ID NO:120, the fragment comprising eight contiguous amino acids of SEQ ID NO:120; and
- (c) the amino acid sequence encoded by the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089;
- the protein being substantially free from other mammalian proteins.

130. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:121;
- (b) the nucleotide sequence of SEQ ID NO:121 from nucleotide 149 to nucleotide 310;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone LL89_3 deposited under accession number ATCC 207089;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:122;

- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122, the fragment comprising eight contiguous amino acids of SEQ ID NO:122;
- 5 (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 10 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:121.

131. A protein comprising an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:122;
- (b) a fragment of the amino acid sequence of SEQ ID NO:122, the fragment comprising eight contiguous amino acids of SEQ ID NO:122; and
- (c) the amino acid sequence encoded by the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089;
- the protein being substantially free from other mammalian proteins.

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132. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:123;
- 25 (b) the nucleotide sequence of SEQ ID NO:123 from nucleotide 22 to nucleotide 288;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone mc300_1 deposited under accession number ATCC 207089;
- 30 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:124;

- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124, the fragment comprising eight contiguous amino acids of SEQ ID NO:124;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:123.

133. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:124;
- (b) a fragment of the amino acid sequence of SEQ ID NO:124, the fragment comprising eight contiguous amino acids of SEQ ID NO:124; and
- (c) the amino acid sequence encoded by the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089;
- the protein being substantially free from other mammalian proteins.

134. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:125;
- (b) the nucleotide sequence of SEQ ID NO:125 from nucleotide 200 to nucleotide 2449;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ml227_1 deposited under accession number ATCC 207089;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:126;

- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126, the fragment comprising eight contiguous amino acids of SEQ ID NO:126;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:125.
135. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:126;
- (b) a fragment of the amino acid sequence of SEQ ID NO:126, the fragment comprising eight contiguous amino acids of SEQ ID NO:126; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089;
- the protein being substantially free from other mammalian proteins.
136. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:127;
- (b) the nucleotide sequence of SEQ ID NO:127 from nucleotide 82 to nucleotide 1980;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone mm367_6 deposited under accession number ATCC 207089;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:128;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128, the fragment comprising eight contiguous amino acids of SEQ ID NO:128;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:127.

137. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:128;

(b) a fragment of the amino acid sequence of SEQ ID NO:128, the fragment comprising eight contiguous amino acids of SEQ ID NO:128; and

(c) the amino acid sequence encoded by the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089; the protein being substantially free from other mammalian proteins.

138. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:129;

(b) the nucleotide sequence of SEQ ID NO:129 from nucleotide 125 to nucleotide 856;

(c) the nucleotide sequence of the full-length protein coding sequence of clone mt124_3 deposited under accession number ATCC 207089;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:130;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:129.

139. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:130;

(b) a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130; and

(c) the amino acid sequence encoded by the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins.

140. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:131;

(b) the nucleotide sequence of SEQ ID NO:131 from nucleotide 856 to nucleotide 2940;

(c) the nucleotide sequence of SEQ ID NO:131 from nucleotide 901 to nucleotide 2940;

(d) the nucleotide sequence of the full-length protein coding sequence of clone nf56_3 deposited under accession number ATCC 207089;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;

(f) the nucleotide sequence of a mature protein coding sequence of clone nf56_3 deposited under accession number ATCC 207089;

- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:132;
- 5 (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132, the fragment comprising eight contiguous amino acids of SEQ ID NO:132;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- 10 (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:131.

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141. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:132;
- (b) a fragment of the amino acid sequence of SEQ ID NO:132, the
- 20 fragment comprising eight contiguous amino acids of SEQ ID NO:132; and
- (c) the amino acid sequence encoded by the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;
- the protein being substantially free from other mammalian proteins.

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142. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:133;
- (b) the nucleotide sequence of SEQ ID NO:133 from nucleotide 122 to nucleotide 448;
- 30 (c) the nucleotide sequence of SEQ ID NO:133 from nucleotide 167 to nucleotide 448;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone qy442_2 deposited under accession number ATCC 207089;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;

5 (f) the nucleotide sequence of a mature protein coding sequence of clone qy442_2 deposited under accession number ATCC 207089;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:134;

10 (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134, the fragment comprising eight contiguous amino acids of SEQ ID NO:134;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

15 (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:133.

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143. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:134;

25 (b) a fragment of the amino acid sequence of SEQ ID NO:134, the fragment comprising eight contiguous amino acids of SEQ ID NO:134; and

(c) the amino acid sequence encoded by the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins.

30 144. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:135;

(b) the nucleotide sequence of SEQ ID NO:135 from nucleotide 28 to nucleotide 777;

- (c) the nucleotide sequence of SEQ ID NO:135 from nucleotide 73 to nucleotide 777;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone rj214_14 deposited under accession number ATCC 207089;
- 5 (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089;
- (f) the nucleotide sequence of a mature protein coding sequence of clone rj214_14 deposited under accession number ATCC 207089;
- 10 (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:136;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136, the fragment comprising eight contiguous amino acids of SEQ ID NO:136;
- 15 (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- 20 (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:135.
- 25 145. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:136;
- (b) a fragment of the amino acid sequence of SEQ ID NO:136, the fragment comprising eight contiguous amino acids of SEQ ID NO:136; and
- 30 (c) the amino acid sequence encoded by the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089;
- the protein being substantially free from other mammalian proteins.

146. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:137;
- (b) the nucleotide sequence of SEQ ID NO:137 from nucleotide 179 to
5 nucleotide 745;
- (c) the nucleotide sequence of SEQ ID NO:137 from nucleotide 233 to
nucleotide 745;
- (d) the nucleotide sequence of the full-length protein coding sequence
of clone rk80_3 deposited under accession number ATCC 207089;
- 10 (e) a nucleotide sequence encoding the full-length protein encoded by
the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;
- (f) the nucleotide sequence of a mature protein coding sequence of
clone rk80_3 deposited under accession number ATCC 207089;
- (g) a nucleotide sequence encoding a mature protein encoded by the
15 cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;
- (h) a nucleotide sequence encoding a protein comprising the amino
acid sequence of SEQ ID NO:138;
- (i) a nucleotide sequence encoding a protein comprising a fragment
of the amino acid sequence of SEQ ID NO:138, the fragment comprising eight
20 contiguous amino acids of SEQ ID NO:138;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees
C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- 25 (k) the nucleotide sequence of a polynucleotide that hybridizes under
conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees
C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and
that has a length that is at least 25% of the length of SEQ ID NO:137.

147. A protein comprising an amino acid sequence selected from the group
30 consisting of:

- (a) the amino acid sequence of SEQ ID NO:138;
- (b) a fragment of the amino acid sequence of SEQ ID NO:138, the
fragment comprising eight contiguous amino acids of SEQ ID NO:138; and

(c) the amino acid sequence encoded by the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089; the protein being substantially free from other mammalian proteins.

- 5 148. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:139;
 - (b) the nucleotide sequence of SEQ ID NO:139 from nucleotide 1017 to nucleotide 1274;
 - 10 (c) the nucleotide sequence of the full-length protein coding sequence of clone au36_42 deposited under accession number ATCC 207187;
 - (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone au36_42 deposited under accession number ATCC 207187;
 - 15 (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:140;
 - (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140, the fragment comprising eight contiguous amino acids of SEQ ID NO:140;
 - 20 (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
 - (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and
 - 25 that has a length that is at least 25% of the length of SEQ ID NO:139.

149. A protein comprising an amino acid sequence selected from the group consisting of:

- 30 (a) the amino acid sequence of SEQ ID NO:140;
- (b) a fragment of the amino acid sequence of SEQ ID NO:140, the fragment comprising eight contiguous amino acids of SEQ ID NO:140; and
- (c) the amino acid sequence encoded by the cDNA insert of clone au36_42 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins.

150. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- 5 (a) the nucleotide sequence of SEQ ID NO:141;
- (b) the nucleotide sequence of SEQ ID NO:141 from nucleotide 580 to nucleotide 774;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone bo549_13 deposited under accession number ATCC 207187;
- 10 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:142;
- 15 (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142, the fragment comprising eight contiguous amino acids of SEQ ID NO:142;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 20 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:141.

25 151. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:142;
- (b) a fragment of the amino acid sequence of SEQ ID NO:142, the
- 30 fragment comprising eight contiguous amino acids of SEQ ID NO:142; and
- (c) the amino acid sequence encoded by the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins.

152. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:143;
- (b) the nucleotide sequence of SEQ ID NO:143 from nucleotide 172 to nucleotide 969;
- (c) the nucleotide sequence of SEQ ID NO:143 from nucleotide 385 to nucleotide 969;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone da529_3 deposited under accession number ATCC 207187;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;
- (f) the nucleotide sequence of a mature protein coding sequence of clone da529_3 deposited under accession number ATCC 207187;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:144;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144, the fragment comprising eight contiguous amino acids of SEQ ID NO:144;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:143.

153. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:144;
- (b) a fragment of the amino acid sequence of SEQ ID NO:144, the fragment comprising eight contiguous amino acids of SEQ ID NO:144; and

(c) the amino acid sequence encoded by the cDNA insert of clone da529_3 deposited under accession number ATCC 207187; the protein being substantially free from other mammalian proteins.

- 5 154. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:145;
 - (b) the nucleotide sequence of SEQ ID NO:145 from nucleotide 329 to nucleotide 667;
 - 10 (c) the nucleotide sequence of SEQ ID NO:145 from nucleotide 368 to nucleotide 667;
 - (d) the nucleotide sequence of the full-length protein coding sequence of clone dm365_3 deposited under accession number ATCC 207187;
 - (e) a nucleotide sequence encoding the full-length protein encoded by
15 the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;
 - (f) the nucleotide sequence of a mature protein coding sequence of clone dm365_3 deposited under accession number ATCC 207187;
 - (g) a nucleotide sequence encoding a mature protein encoded by the
20 cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;
 - (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:146;
 - (i) a nucleotide sequence encoding a protein comprising a fragment
25 of the amino acid sequence of SEQ ID NO:146, the fragment comprising eight contiguous amino acids of SEQ ID NO:146;
 - (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
 - (k) the nucleotide sequence of a polynucleotide that hybridizes under
30 conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:145.

155. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:146;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:146, the
5 fragment comprising eight contiguous amino acids of SEQ ID NO:146; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;
- the protein being substantially free from other mammalian proteins.

10 156. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:147;
- (b) the nucleotide sequence of SEQ ID NO:147 from nucleotide 103 to
nucleotide 1368;
- 15 (c) the nucleotide sequence of the full-length protein coding sequence of clone fa171_1 deposited under accession number ATCC 207187;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187;
- 20 (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:148;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148, the fragment comprising eight contiguous amino acids of SEQ ID NO:148;
- 25 (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under
30 conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:147.

157. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:148;
(b) a fragment of the amino acid sequence of SEQ ID NO:148, the fragment comprising eight contiguous amino acids of SEQ ID NO:148; and
(c) the amino acid sequence encoded by the cDNA insert of clone
5 fa171_1 deposited under accession number ATCC 207187;
the protein being substantially free from other mammalian proteins.

158. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- 10 (a) the nucleotide sequence of SEQ ID NO:149;
(b) the nucleotide sequence of SEQ ID NO:149 from nucleotide 190 to nucleotide 1407;
(c) the nucleotide sequence of SEQ ID NO:149 from nucleotide 463 to nucleotide 1407;
15 (d) the nucleotide sequence of the full-length protein coding sequence of clone lp572_2 deposited under accession number ATCC 207187;
(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187;
20 (f) the nucleotide sequence of a mature protein coding sequence of clone lp572_2 deposited under accession number ATCC 207187;
(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187;
(h) a nucleotide sequence encoding a protein comprising the amino
25 acid sequence of SEQ ID NO:150;
(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150, the fragment comprising eight contiguous amino acids of SEQ ID NO:150;
(j) the nucleotide sequence of a polynucleotide that hybridizes under
30 conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:149.

159. A protein comprising an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:150;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:150, the fragment comprising eight contiguous amino acids of SEQ ID NO:150; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 lp572_2 deposited under accession number ATCC 207187;
- the protein being substantially free from other mammalian proteins.

160. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- 15 (a) the nucleotide sequence of SEQ ID NO:151;
- (b) the nucleotide sequence of SEQ ID NO:151 from nucleotide 301 to nucleotide 1035;
- (c) the nucleotide sequence of SEQ ID NO:151 from nucleotide 916 to nucleotide 1035;
- 20 (d) the nucleotide sequence of the full-length protein coding sequence of clone pe246_1 deposited under accession number ATCC 207187;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;
- 25 (f) the nucleotide sequence of a mature protein coding sequence of clone pe246_1 deposited under accession number ATCC 207187;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;
- (h) a nucleotide sequence encoding a protein comprising the amino
30 acid sequence of SEQ ID NO:152;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152, the fragment comprising eight contiguous amino acids of SEQ ID NO:152;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

5 (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:151.

10 161. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:152;

(b) a fragment of the amino acid sequence of SEQ ID NO:152, the fragment comprising eight contiguous amino acids of SEQ ID NO:152; and

15 (c) the amino acid sequence encoded by the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins.

162. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

20 (a) the nucleotide sequence of SEQ ID NO:153;

(b) the nucleotide sequence of SEQ ID NO:153 from nucleotide 94 to nucleotide 1281;

(c) the nucleotide sequence of the full-length protein coding sequence of clone qf122_3 deposited under accession number ATCC 207187;

25 (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:154;

30 (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154, the fragment comprising eight contiguous amino acids of SEQ ID NO:154;

- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- 5 (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:153.

10 163. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:154;
- (b) a fragment of the amino acid sequence of SEQ ID NO:154, the fragment comprising eight contiguous amino acids of SEQ ID NO:154; and
- 15 (c) the amino acid sequence encoded by the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187;
- the protein being substantially free from other mammalian proteins.

164. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- 20 (a) the nucleotide sequence of SEQ ID NO:155;
- (b) the nucleotide sequence of SEQ ID NO:155 from nucleotide 110 to nucleotide 742;
- (c) the nucleotide sequence of SEQ ID NO:155 from nucleotide 170 to nucleotide 742;
- 25 (d) the nucleotide sequence of the full-length protein coding sequence of clone qv538_1 deposited under accession number ATCC 207187;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;
- 30 (f) the nucleotide sequence of a mature protein coding sequence of clone qv538_1 deposited under accession number ATCC 207187;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;

- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:156;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156, the fragment comprising eight contiguous amino acids of SEQ ID NO:156;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:155.
165. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:156;
- (b) a fragment of the amino acid sequence of SEQ ID NO:156, the fragment comprising eight contiguous amino acids of SEQ ID NO:156; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;
- the protein being substantially free from other mammalian proteins.
166. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:157;
- (b) the nucleotide sequence of SEQ ID NO:157 from nucleotide 41 to nucleotide 757;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ys20_1 deposited under accession number ATCC 207187;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:158;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158, the fragment comprising eight contiguous amino acids of SEQ ID NO:158;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:157.

167. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:158;

(b) a fragment of the amino acid sequence of SEQ ID NO:158, the fragment comprising eight contiguous amino acids of SEQ ID NO:158; and

(c) the amino acid sequence encoded by the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins.

168. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:159;

(b) the nucleotide sequence of SEQ ID NO:159 from nucleotide 28 to nucleotide 2253;

(c) the nucleotide sequence of SEQ ID NO:159 from nucleotide 568 to nucleotide 2253;

(d) the nucleotide sequence of the full-length protein coding sequence of clone as180_1 deposited under accession number ATCC XXXXXX;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;

(f) the nucleotide sequence of a mature protein coding sequence of clone as180_1 deposited under accession number ATCC XXXXXX;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:160;

5 (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160, the fragment comprising eight contiguous amino acids of SEQ ID NO:160;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees
10 C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:159.

15

169. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:160;

(b) a fragment of the amino acid sequence of SEQ ID NO:160, the
20 fragment comprising eight contiguous amino acids of SEQ ID NO:160; and

(c) the amino acid sequence encoded by the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;

the protein being substantially free from other mammalian proteins.

Fig. 1A

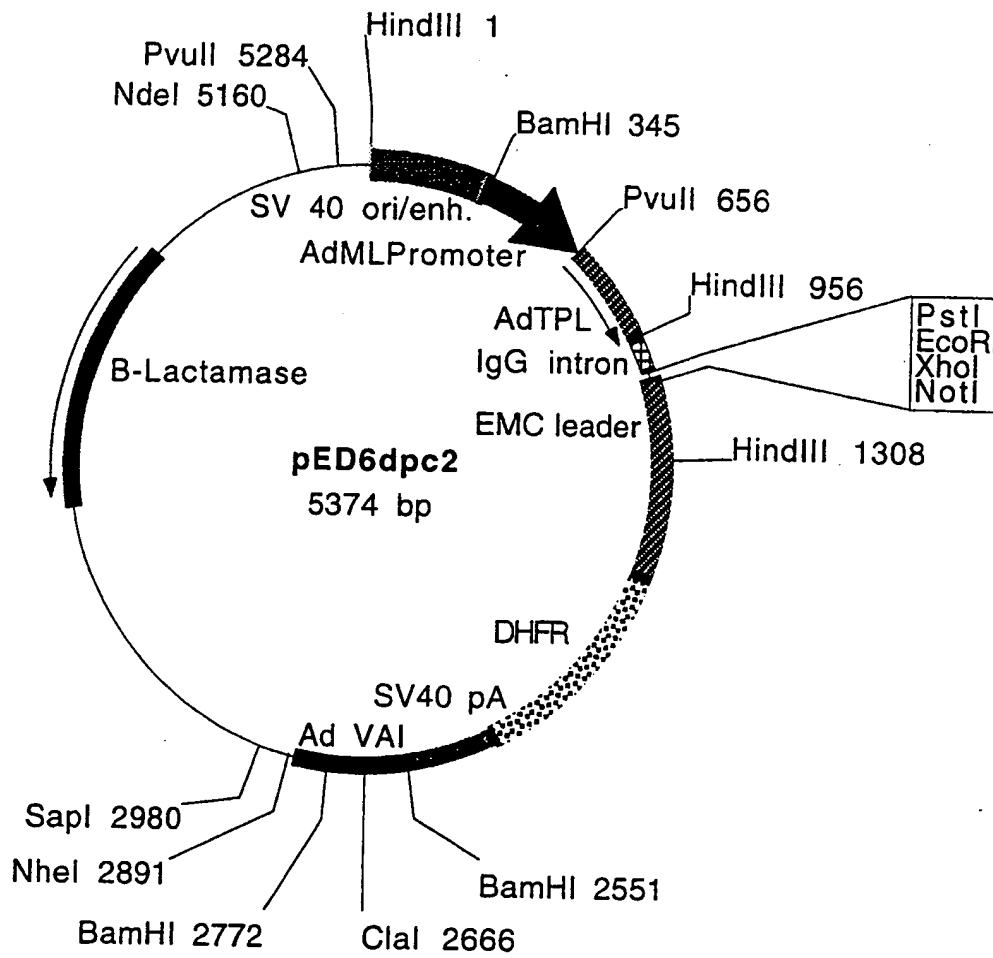


Fig. 1B

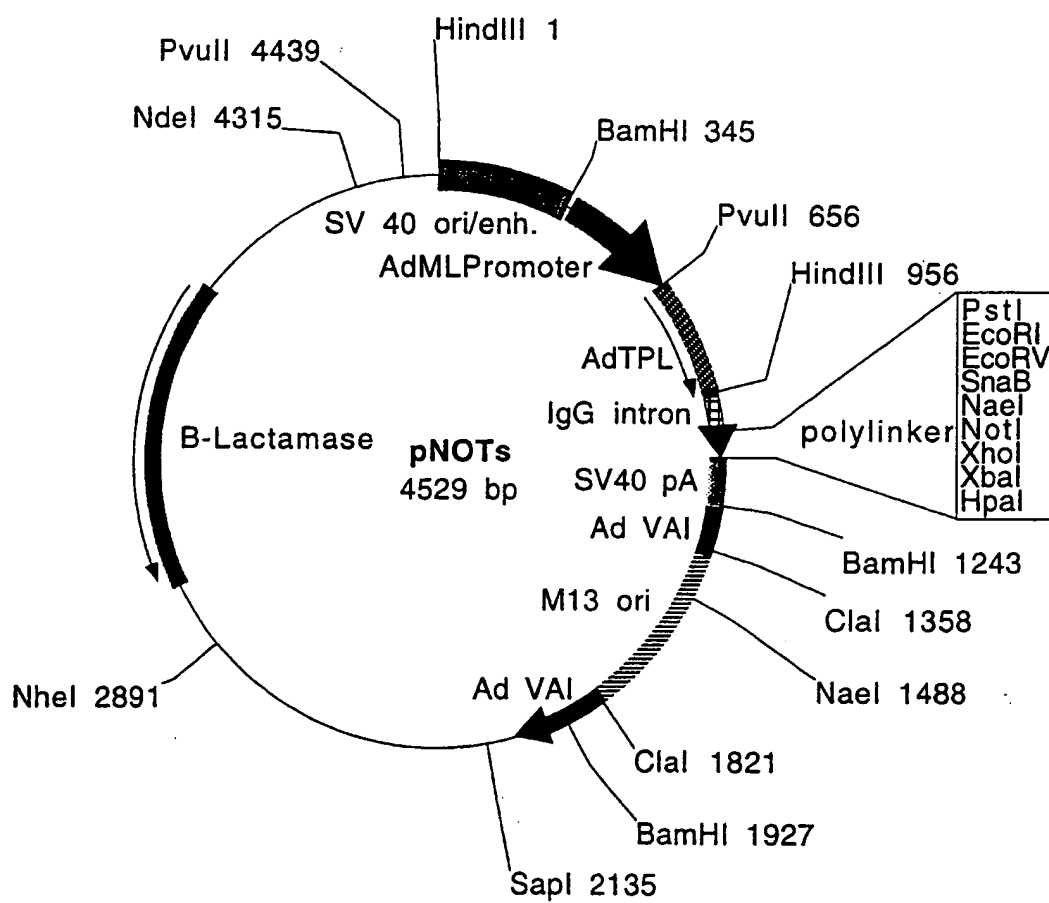
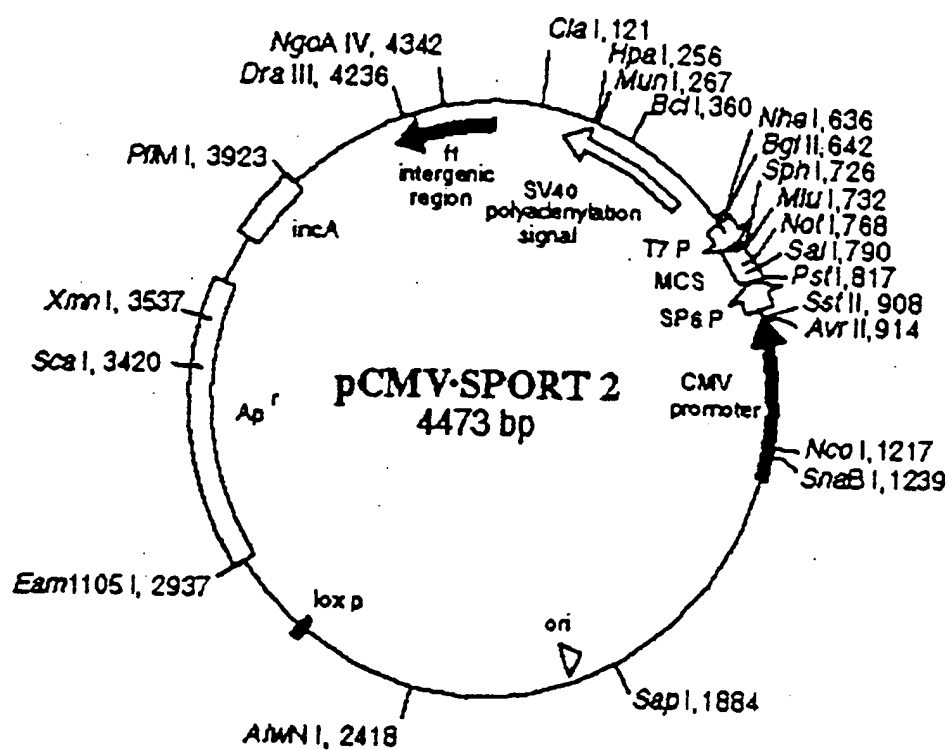


Fig. 2



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Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile Val Met Phe Thr Ala
      65              70              75              80

Leu Gln Leu His Arg Gln Cys Val Val Cys Lys Gln Ala Asp Glu Glu
      85              90              95

Phe Gln Ile Leu Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Thr Asn
      100             105             110

Arg Ile Phe Phe Ala Met Val Asp Phe Asp Glu Gly Ser Asp Val Phe
      115             120             125

Gln Met Leu Asn Met Asn Ser Ala Pro Thr Phe Ile Asn Phe Pro Ala
      130             135             140

Lys Gly Lys Pro Lys Arg Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly
      145             150             155             160

Phe Ser Ala Glu Gln Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val
      165             170             175

Asn Ile Arg Val Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu
      180             185             190

Gly Leu Leu Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser
      195             200             205

Asn Met Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu
      210             215             220

Cys Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
      225             230             235             240

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Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn Tyr
 245 250 255

Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His Ile Val
 260 265 270

Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu Leu Cys Glu
 275 280 285

Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys Ile Met Cys Val
 290 295 300

Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser Trp Met Leu Ser Ile
 305 310 315 320

Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr Ser Phe Leu Met Ser
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<210> 5

<211> 1697

<212> DNA

<213> Homo sapiens

<400> 5

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1697

<210> 6

<211> 158

<212> PRT

<213> Homo sapiens

<400> 6

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Glu Leu Glu Ile Ser Gly Lys Val Arg Ser Leu Ser Ala Ser Leu Trp
 35 40 45

Ser Leu Thr His Leu Thr Ala Leu His Leu Ser Asp Asn Ser Leu Ser
 50 55 60

Arg Ile Pro Ser Asp Ile Ala Lys Leu His Asn Leu Val Tyr Leu Asp
 65 70 75 80

Leu Ser Ser Asn Lys Ile Arg Ser Leu Pro Ala Glu Leu Gly Asn Met
 85 90 95

Val Ser Leu Arg Glu Leu His Leu Asn Asn Asn Leu Leu Arg Val Leu
 100 105 110

Pro Phe Glu Leu Gly Lys Leu Phe Gln Leu Gln Thr Leu Gly Leu Lys
 115 120 125

Gly Met Thr Ser Ile Phe Val Leu Leu Met Val Cys Val Tyr Val Phe
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Glu Ser Lys Glu Ala Lys Lys Leu Ser Ala Arg Gly Phe Phe
 145 150 155

<210> 7

<211> 1462

<212> DNA

<213> Homo sapiens

<400> 7

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<211> 248

<212> PRT

<213> Homo sapiens

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 20 25 30

Arg Leu Pro Ser Lys Cys Glu Val Cys Lys Leu Leu Ser Thr Glu Leu
 35 40 45

Gln Ala Glu Leu Ser Arg Thr Gly Arg Ser Arg Glu Val Leu Glu Leu
 50 55 60

Gly Gln Val Leu Asp Thr Gly Lys Arg Lys Arg His Val Pro Tyr Ser
 65 70 75 80

Val Ser Glu Thr Arg Leu Glu Glu Ala Leu Glu Asn Leu Cys Glu Arg
 85 90 95

Ile Leu Asp Tyr Ser Val His Ala Glu Arg Lys Gly Ser Leu Arg Tyr
 100 105 110

Ala Lys Gly Gln Ser Gln Thr Met Ala Thr Leu Lys Gly Leu Val Gln
 115 120 125

Lys Gly Val Lys Val Asp Leu Gly Ile Pro Leu Glu Leu Trp Asp Glu
 130 135 140

Pro Ser Val Glu Val Thr Tyr Leu Lys Lys Gln Cys Glu Thr Met Leu
 145 150 155 160

Glu Glu Phe Glu Asp Ile Val Gly Asp Trp Tyr Phe His His Gln Glu
 165 170 175

Gln Pro Leu Gln Asn Phe Leu Cys Glu Gly His Val Leu Pro Ala Ala
 180 185 190

Glu Thr Ala Cys Leu Gln Glu Thr Trp Thr Gly Lys Glu Ile Thr Asp
 195 200 205

Gly Glu Glu Lys Thr Glu Gly Glu Glu Glu Gln Glu Glu Glu Glu
 210 215 220

Glu Glu Glu Glu Glu Gly Gly Asp Lys Met Thr Lys Thr Gly Ser His
 225 230 235 240

Pro Lys Leu Asp Arg Glu Asp Leu
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<210> 9

<211> 2104

<212> DNA

<213> Homo sapiens

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<210> 10

<211> 373

<212> PRT

<213> Homo sapiens

<400> 10

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      20              25              30

Gly Gln Lys Lys Ile Arg Glu Ile Gln Glu Arg Glu Ala Ala Glu Tyr
      35              40              45

Ile Ala Gln Ala Arg Arg Gln Tyr His Phe Glu Ser Asn Gln Arg Thr
      50              55              60

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Cys Asn Met Thr Val Leu Ser Met Leu Pro Thr Leu Arg Glu Ala Leu
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 Met Gln Gln Leu Asn Ser Glu Ser Leu Thr Ala Leu Leu Lys Asn Arg
 85 90 95
 Pro Ser Asn Lys Leu Glu Ile Trp Glu Asp Leu Lys Ile Ile Ser Phe
 100 105 110
 Thr Arg Ser Thr Val Ala Val Tyr Ser Thr Cys Met Leu Val Val Leu
 115 120 125
 Leu Arg Val Gln Leu Asn Ile Ile Gly Gly Tyr Ile Tyr Leu Asp Asn
 130 135 140
 Ala Ala Val Gly Lys Asn Gly Thr Thr Ile Leu Ala Pro Pro Asp Val
 145 150 155 160
 Gln Gln Gln Tyr Leu Ser Ser Ile Gln His Leu Leu Gly Asp Gly Leu
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 Thr Glu Leu Ile Thr Val Ile Lys Gln Ala Val Gln Lys Val Leu Gly
 180 185 190
 Ser Val Ser Leu Lys His Ser Leu Ser Leu Leu Asp Leu Glu Gln Lys
 195 200 205
 Leu Lys Glu Ile Arg Asn Leu Val Glu Gln His Lys Ser Ser Ser Trp
 210 215 220
 Ile Asn Lys Asp Gly Ser Lys Pro Leu Leu Cys His Tyr Met Met Pro
 225 230 235 240
 Asp Glu Glu Thr Pro Leu Ala Val Gln Ala Cys Gly Leu Ser Pro Arg
 245 250 255
 Asp Ile Thr Thr Ile Lys Leu Leu Asn Glu Thr Arg Asp Met Leu Glu
 260 265 270
 Ser Pro Asp Phe Ser Thr Val Leu Asn Thr Cys Leu Asn Arg Gly Phe
 275 280 285
 Ser Arg Leu Leu Asp Asn Met Ala Glu Phe Phe Arg Pro Thr Glu Gln
 290 295 300
 Asp Leu Gln His Gly Asn Ser Met Asn Ser Leu Ser Ser Val Ser Leu
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 Pro Leu Ala Lys Ile Ile Pro Ile Val Asn Gly Gln Ile His Ser Val
 325 330 335
 Cys Ser Glu Thr Pro Ser His Phe Val Gln Asp Leu Leu Thr Met Glu
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 Gln Val Lys Asp Phe Ala Ala Asn Val Tyr Glu Ala Phe Ser Thr Pro
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<210> 11
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 <212> DNA
 <213> Homo sapiens

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<210> 12

<211> 837

<212> PRT

<213> Homo sapiens

<400> 12

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Pro Gly Ala Pro Arg Ala Ala Ala Gly Leu Leu Pro Gly Gly Lys Ala
35 40 45

Arg Glu Phe Asn Arg Asn Gln Arg Lys Asp Ser Glu Gly Tyr Ser Glu
50 55 60

Ser Pro Asp Leu Glu Phe Glu Tyr Ala Asp Thr Asp Lys Trp Ala Ala
65 70 75 80

Glu Leu Ser Glu Leu Tyr Ser Tyr Thr Glu Gly Pro Glu Phe Leu Met
85 90 95

Asn Arg Lys Cys Phe Glu Glu Asp Phe Arg Ile His Val Thr Asp Lys
100 105 110

Lys Trp Thr Glu Leu Asp Thr Asn Gln His Arg Thr His Ala Met Arg
115 120 125

Leu Leu Asp Gly Leu Glu Val Thr Ala Arg Glu Lys Arg Leu Lys Val
130 135 140

Ala Arg Ala Ile Leu Tyr Val Ala Gln Gly Thr Phe Gly Glu Cys Ser
145 150 155 160

Ser Glu Ala Glu Val Gln Ser Trp Met Arg Tyr Asn Ile Phe Leu Leu
165 170 175

Leu Glu Val Gly Thr Phe Asn Ala Leu Val Glu Leu Leu Asn Met Glu
180 185 190

Ile Asp Asn Ser Ala Ala Cys Ser Ser Ala Val Arg Lys Pro Ala Ile
195 200 205

Ser Leu Ala Asp Ser Thr Asp Leu Arg Val Leu Leu Asn Ile Met Tyr
210 215 220

Leu Ile Val Glu Thr Val His Gln Glu Cys Glu Gly Asp Lys Ala Glu
225 230 235 240

Trp Arg Thr Met Arg Gln Thr Phe Arg Ala Glu Leu Gly Ser Pro Leu
245 250 255

Tyr Asn Asn Glu Pro Phe Ala Ile Met Leu Phe Gly Met Val Thr Lys
260 265 270

Phe Cys Ser Gly His Ala Pro His Phe Pro Met Lys Lys Val Leu Leu
 275 280 285
 Leu Leu Trp Lys Thr Val Leu Cys Thr Leu Gly Gly Phe Glu Glu Leu
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 Pro Glu Asp Ser Ile Lys Val Ile Arg Asn Met Arg Ala Ala Ser Pro
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 Leu Leu Pro Ser Leu Pro Gln Tyr Met Ile Ala Leu Leu Lys Ile Leu
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 Leu Ala Ala Ala Pro Thr Ser Lys Ala Lys Thr Asp Ser Ile Asn Ile
 530 535 540
 Leu Ala Asp Val Leu Pro Glu Glu Met Pro Thr Thr Val Leu Gln Ser
 545 550 555 560
 Met Lys Leu Gly Val Asp Val Asn Arg His Lys Glu Val Ile Val Lys
 565 570 575
 Ala Ile Ser Ala Val Leu Leu Leu Leu Lys His Phe Lys Leu Asn
 580 585 590

His Val Tyr Gln Phe Glu Tyr Met Ala Gln His Leu Val Phe Ala Asn
 595 600 605

Cys Ile Pro Leu Ile Leu Lys Phe Phe Asn Gln Asn Ile Met Ser Tyr
 610 615 620

Ile Thr Ala Lys Asn Ser Ile Ser Val Leu Asp Tyr Pro His Cys Val
 625 630 635 640

Val His Glu Leu Pro Glu Leu Thr Ala Glu Ser Leu Glu Ala Gly Asp
 645 650 655

Ser Asn Gln Phe Cys Trp Arg Asn Leu Phe Ser Cys Ile Asn Leu Leu
 660 665 670

Arg Ile Leu Asn Lys Leu Thr Lys Trp Lys His Ser Arg Thr Met Met
 675 680 685

Leu Val Val Phe Lys Ser Ala Pro Ile Leu Lys Arg Ala Leu Lys Val
 690 695 700

Lys Gln Ala Met Met Gln Leu Tyr Val Leu Lys Leu Leu Lys Val Gln
 705 710 715 720

Thr Lys Tyr Leu Gly Arg Gln Trp Arg Lys Ser Asn Met Lys Thr Met
 725 730 735

Ser Ala Ile Tyr Gln Lys Val Arg His Arg Leu Asn Asp Asp Trp Ala
 740 745 750

Tyr Gly Asn Asp Leu Asp Ala Arg Pro Trp Asp Phe Gln Ala Glu Glu
 755 760 765

Cys Ala Leu Arg Ala Asn Ile Glu Arg Phe Asn Ala Arg Arg Tyr Asp
 770 775 780

Arg Ala His Ser Asn Pro Asp Phe Leu Pro Val Asp Asn Cys Leu Gln
 785 790 795 800

Ser Val Leu Gly Gln Arg Val Asp Leu Pro Glu Asp Phe Gln Met Asn
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Tyr Asp Leu Trp Leu Glu Arg Glu Val Phe Ser Lys Pro Ile Ser Trp
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Glu Glu Leu Leu Gln
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<210> 13

<211> 1264

<212> DNA

<213> Homo sapiens

<400> 13

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 acacaagcca agatttcagg caaacaatga gcaagaaata tcccttcac ttggaagttt 180
 attacaaatc cactgagaag tctggaatgt atggaatcag agagctagat caaaaaacat 240
 ggttgaacag caaaaattag atgtaaggaa gatctgcatt caaatgtgag tgggcacat 300

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cagaacagcg tgggcaacg tgtttagtct ccttaaaagg atttactct gtcaccagg 480
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attttttggg gtttttagtg gagacagggt ttcacogtgt tggccagggt ggtctcgaac 660
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<210> 14

<211> 80

<212> PRT

<213> Homo sapiens

<400> 14

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Met Ala Arg Thr Leu Glu Pro Leu Ala Lys Lys Ile Phe Lys Gly Val
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Leu Val Ala Glu Leu Val Gly Val Phe Gly Ala Tyr Phe Leu Phe Ser
             20             25             30
Lys Met His Thr Ser Gln Asp Phe Arg Gln Thr Met Ser Lys Lys Tyr
             35             40             45
Pro Phe Ile Leu Glu Val Tyr Tyr Lys Ser Thr Glu Lys Ser Gly Met
             50             55             60
Tyr Gly Ile Arg Glu Leu Asp Gln Lys Thr Trp Leu Asn Ser Lys Asn
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<210> 15

<211> 2671

<212> DNA

<213> Homo sapiens

<400> 15

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<210> 16

<211> 804

<212> PRT

<213> Homo sapiens

<400> 16

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Met Ala Ala His Arg Pro Gly Pro Leu Lys Gln Gln Asn Lys Ala His
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Lys Gly Gly Arg His Arg Gly Arg Gly Ser Ala Gln Arg Asp Gly Lys
      20              25              30

```

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Gly Arg Leu Ala Leu Lys Thr Leu Ser Lys Lys Val Arg Lys Glu Leu
      35              40              45

```

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Ser Arg Val Asp Gln Arg His Arg Ala Ser Gln Leu Arg Lys Gln Lys
      50              55              60

```

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Lys Glu Ala Val Leu Ala Glu Lys Arg Gln Leu Gly Gly Lys Asp Gly
      65              70              75              80

```

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Pro Pro His Gln Val Leu Val Val Pro Leu His Ser Arg Ile Ser Leu
      85              90              95

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```

Pro Glu Ala Met Gln Leu Leu Gln Asp Arg Asp Thr Gly Thr Val His
      100             105             110

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Leu Asn Glu Leu Gly Asn Thr Gln Asn Phe Met Leu Leu Cys Pro Arg

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115	120	125
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130	135	140
Val Val Leu Asp Met Ala Lys Val Ala Asp Thr Ile Leu Phe Leu Leu		
145	150	155
Asp Pro Leu Glu Gly Trp Asp Ser Thr Arg Asp Tyr Cys Leu Ser Cys		
	165	170
Leu Phe Ala Gln Gly Leu Pro Thr Tyr Thr Leu Ala Val Gln Gly Ile		
	180	185
Ser Gly Leu Pro Leu Lys Lys Gln Ile Asp Thr Arg Lys Lys Leu Ser		
	195	200
Lys Ala Val Glu Lys Arg Phe Pro His Asp Lys Leu Leu Leu Leu Asp		
	210	215
Thr Gln Gln Glu Ala Gly Met Leu Leu Arg Gln Leu Ala Asn Gln Lys		
	225	230
Gln Gln His Leu Ala Phe Arg Asp Arg Arg Ala Tyr Leu Phe Ala His		
	245	250
Ala Val Asp Phe Val Pro Ser Glu Glu Asn Asn Leu Val Gly Thr Leu		
	260	265
Lys Ile Ser Gly Tyr Val Arg Gly Gln Thr Leu Asn Val Asn Arg Leu		
	275	280
Leu His Ile Val Gly Tyr Gly Asp Leu Pro Asp Glu Gln Ile Asp Ala		
	290	295
Pro Gly Asp Pro Phe Pro Leu Asn Pro Arg Gly Ile Lys Pro Gln Lys		
	305	310
Asp Pro Asp Met Ala Met Glu Ile Cys Ala Thr Asp Ala Val Asp Asp		
	325	330
Met Glu Glu Gly Leu Lys Val Leu Met Lys Ala Asp Pro Gly Arg Gln		
	340	345
Glu Ser Leu Gln Ala Glu Val Ile Pro Asp Pro Met Glu Gly Glu Gln		
	355	360
Thr Trp Pro Thr Glu Glu Glu Leu Ser Glu Ala Lys Asp Phe Leu Lys		
	370	375
Glu Ser Ser Lys Val Val Lys Lys Val Pro Lys Gly Thr Ser Ser Tyr		
	385	390
Gln Ala Glu Trp Ile Leu Asp Gly Gly Ser Gln Ser Gly Gly Glu Gly		
	405	410
Asp Glu Tyr Glu Tyr Asp Asp Met Glu His Glu Asp Phe Met Glu Glu		
	420	425
Glu Ser Gln Asp Glu Ser Ser Glu Glu Glu Glu Tyr Glu Thr Met		

435	440	445
Thr Ile Gly Glu Ser Val His Asp Asp Leu Tyr Asp Lys Lys Val Asp 450	455	460
Glu Glu Ala Glu Ala Lys Met Leu Glu Lys Tyr Lys Gln Glu Arg Leu 465	470	475 480
Glu Glu Met Phe Pro Asp Glu Val Asp Thr Pro Arg Asp Val Ala Ala 485	490	495
Arg Ile Arg Phe Gln Lys Tyr Arg Gly Leu Lys Ser Phe Arg Thr Ser 500	505	510
Pro Trp Asp Pro Lys Glu Asn Leu Pro Gln Asp Tyr Ala Arg Ile Phe 515	520	525
Gln Phe Gln Asn Phe Thr Asn Thr Arg Lys Ser Ile Phe Lys Glu Val 530	535	540
Glu Glu Lys Glu Val Glu Gly Ala Glu Val Gly Trp Tyr Val Thr Leu 545	550	555 560
His Val Ser Glu Val Pro Val Ser Val Val Glu Cys Phe Arg Gln Gly 565	570	575
Thr Pro Leu Ile Ala Phe Ser Leu Leu Pro His Glu Gln Lys Met Ser 580	585	590
Val Leu Asn Met Val Val Arg Arg Asp Pro Gly Asn Thr Glu Pro Val 595	600	605
Lys Ala Lys Glu Glu Leu Ile Phe His Cys Gly Phe Arg Arg Phe Arg 610	615	620
Ala Ser Pro Leu Phe Ser Gln His Thr Ala Ala Asp Lys His Lys Leu 625	630	635 640
Gln Arg Phe Leu Thr Ala Asp Met Ala Leu Val Ala Thr Val Tyr Ala 645	650	655
Pro Ile Thr Phe Pro Pro Ala Ser Val Leu Leu Phe Lys Gln Lys Ser 660	665	670
Asn Gly Met His Ser Leu Ile Ala Thr Gly His Leu Met Ser Val Asp 675	680	685
Pro Asp Arg Met Val Ile Lys Arg Val Val Leu Ser Gly His Pro Phe 690	695	700
Lys Ile Phe Thr Lys Met Ala Val Val Arg Tyr Met Phe Phe Asn Arg 705	710	715 720
Glu Asp Val Leu Trp Phe Lys Pro Val Glu Leu Arg Thr Lys Trp Gly 725	730	735
Arg Arg Gly His Ile Lys Glu Pro Leu Gly Thr His Gly His Met Lys 740	745	750
Cys Ser Phe Asp Gly Lys Leu Lys Ser Gln Asp Thr Val Leu Met Asn		

755

760

765

Leu Tyr Lys Arg Val Phe Pro Lys Trp Thr Tyr Asp Pro Tyr Val Pro
 770 775 780

Glu Pro Val Pro Trp Leu Lys Ser Glu Ile Ser Ser Thr Val Pro Gln
 785 790 795 800

Gly Gly Met Glu

<210> 17

<211> 2321

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18

<211> 589

<212> PRT

<213> Homo sapiens

<400> 18

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Ala Lys Leu Gln Pro Trp Ala Trp Thr Leu Lys Arg Ile Gly Gly Gln
      20           25           30

Phe Gly Ala Gly Thr Glu Ser Tyr Phe Ser Leu Leu Arg Phe Leu Leu
 35           40           45

Leu Leu Asn Val Leu Ala Ser Val Leu Met Ala Cys Met Thr Leu Leu
 50           55           60

Pro Thr Trp Leu Gly Gly Ala Pro Pro Gly Pro Pro Gly Pro Asp Ile
 65           70           75           80

Ser Ser Pro Cys Gly Ser Tyr Asn Pro His Ser Gln Gly Leu Val Thr
      85           90           95

Phe Ala Thr Gln Leu Phe Asn Leu Leu Ser Gly Glu Gly Tyr Leu Glu
      100           105           110

Trp Ser Pro Leu Phe Tyr Gly Phe Tyr Thr Pro Arg Pro Arg Leu Ala
 115           120           125

Val Thr Tyr Leu Cys Trp Ala Phe Ala Val Gly Leu Ile Cys Leu Leu
 130           135           140

Leu Ile Leu His Arg Ser Val Ser Gly Leu Lys Gln Thr Leu Leu Ala
 145           150           155           160

Glu Ser Glu Ala Leu Thr Ser Tyr Ser His Arg Val Phe Ser Ala Trp
      165           170           175

Asp Phe Gly Leu Cys Gly Asp Val His Val Arg Leu Arg Gln Arg Ile
 180           185           190

Ile Leu Tyr Glu Leu Lys Val Glu Leu Glu Glu Thr Val Val Arg Arg
 195           200           205

Gln Ala Ala Val Arg Thr Leu Gly Gln Gln Ala Arg Val Trp Leu Val
 210           215           220

Arg Val Leu Leu Asn Leu Leu Val Val Ala Leu Leu Gly Ala Ala Phe
 225           230           235           240

Tyr Gly Val Tyr Trp Ala Thr Gly Cys Thr Val Glu Leu Gln Glu Met
      245           250           255

Pro Leu Val Gln Glu Leu Pro Leu Leu Lys Leu Gly Val Asn Tyr Leu
      260           265           270

Pro Ser Ile Phe Ile Ala Gly Val Asn Phe Val Leu Pro Pro Val Phe
      275           280           285

Lys Leu Ile Ala Pro Leu Glu Gly Tyr Thr Arg Ser Arg Gln Ile Val
 290           295           300

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Phe Ile Leu Leu Arg Thr Val Phe Leu Arg Leu Ala Ser Leu Val Val
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 Ala Glu Asp Cys Lys Thr Cys Gly Tyr Asn Tyr Lys Gln Leu Pro Cys
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 Trp Glu Thr Val Leu Gly Gln Glu Met Tyr Lys Leu Leu Leu Phe Asp
 355 360 365
 Leu Leu Thr Val Leu Ala Val Ala Leu Leu Ile Gln Phe Pro Arg Lys
 370 375 380
 Leu Leu Cys Gly Leu Cys Pro Gly Ala Leu Gly Leu Leu Ala Gly Thr
 385 390 395 400
 Gln Glu Phe Gln Val Pro Asp Glu Val Leu Gly Leu Ile Tyr Ala Gln
 405 410 415
 Thr Val Val Trp Val Gly Ser Phe Phe Cys Pro Leu Leu Pro Leu Leu
 420 425 430
 Asn Thr Val Lys Phe Leu Leu Leu Phe Tyr Leu Lys Lys Leu Thr Leu
 435 440 445
 Phe Ser Thr Cys Ser Pro Ala Ala Arg Thr Phe Arg Ala Ser Ala Ala
 450 455 460
 Asn Phe Phe Phe Pro Leu Val Leu Leu Leu Gly Leu Ala Ile Ser Ser
 465 470 475 480
 Val Pro Leu Leu Tyr Ser Ile Phe Leu Ile Pro Pro Ser Lys Leu Cys
 485 490 495
 Gly Pro Phe Arg Gly Gln Ser Ser Ile Trp Ala Gln Ile Pro Glu Ser
 500 505 510
 Ile Ser Ser Leu Pro Glu Thr Thr Gln Asn Phe Leu Phe Phe Leu Gly
 515 520 525
 Thr Gln Ala Phe Ala Val Pro Leu Leu Leu Ile Ser Ser Ile Leu Met
 530 535 540
 Ala Tyr Thr Val Ala Leu Ala Asn Ser Tyr Gly Arg Leu Ile Ser Glu
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 Arg Arg Ala Val Ala Leu Thr Ser Thr Lys Pro Ala Leu
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<210> 19

<211> 5263

<212> DNA

<213> Homo sapiens

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<210> 26

<211> 545

<212> PRT

<213> Homo sapiens

<400> 26

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His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser
      35           40           45

Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys
 50           55           60

Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile
 65           70           75           80

Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp
      85           90           95

Gly Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp
      100           105           110

Thr Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp
      115           120           125

Val Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr Lys
      130           135           140

Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe
      145           150           155           160

Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg
      165           170           175

Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu
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Val Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr
      195           200           205

Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu
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Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro
      225           230           235           240

Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln
      245           250           255

Ile Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu Asp
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Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr
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Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala
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 385 390 395 400
 Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser
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 Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys
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 Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met
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Asp
 545

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 <213> Homo sapiens

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<210> 28

<211> 591

<212> PRT

<213> Homo sapiens

<400> 28

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Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu Leu His Ser Ser Lys Trp 35 40 45		
Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala Leu Pro Leu Ala Glu Leu 50 55 60		
Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp Ala Gln Asp Met Asp Ala 65 70 75 80		
Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val Lys Glu Tyr Asp Arg Ala 85 90 95		
Ala His Phe Leu His Gly Cys Asn Ser Lys Lys Ala Tyr Phe Leu Tyr 100 105 110		
Met Tyr Ser Arg Tyr Leu Ser Gly Glu Lys Lys Lys Asp Asp Glu Thr 115 120 125		
Val Asp Ser Leu Gly Pro Leu Glu Lys Gly Gln Val Lys Asn Glu Ala 130 135 140		
Leu Arg Glu Leu Arg Val Glu Leu Ser Lys Lys His Gln Ala Arg Glu 145 150 155 160		
Leu Asp Gly Phe Gly Leu Tyr Leu Tyr Gly Val Val Leu Arg Lys Leu 165 170 175		
Asp Leu Val Lys Glu Ala Ile Asp Val Phe Val Glu Ala Thr His Val 180 185 190		
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Asp Lys Tyr Arg Val Glu Thr Cys Cys Val Ile Gly Asn Tyr Tyr Ser 325 330 335		
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Lys Leu Asn Pro Arg Tyr Leu Gly Ala Trp Thr Leu Met Gly His Glu 355	360	365
Tyr Met Glu Met Lys Asn Thr Ser Ala Ala Ile Gln Ala Tyr Arg His 370	375	380
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Gln Thr Tyr Glu Ile Leu Lys Met Pro Phe Tyr Cys Leu Tyr Tyr Tyr 405	410	415
Arg Arg Ala His Gln Leu Arg Pro Asn Asp Ser Arg Met Leu Val Ala 420	425	430
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Cys Phe Trp Ile Ala Tyr Ala Val Gly Asp Val Glu Lys Met Ala Leu 450	455	460
Val Lys Leu Ala Lys Leu His Glu Gln Leu Thr Glu Ser Glu Gln Ala 465	470	475 480
Ala Gln Cys Tyr Ile Lys Tyr Ile Gln Asp Ile Tyr Thr Cys Gly Glu 485	490	495
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Tyr Tyr Phe Lys Cys Lys Leu Trp Asp Glu Ala Ser Thr Cys Ala Gln 515	520	525
Lys Cys Cys Ala Phe Asn Asp Thr Arg Glu Glu Gly Lys Ala Leu Leu 530	535	540
Arg Gln Ile Leu Gln Leu Arg Asn Gln Gly Glu Thr Pro Thr Thr Glu 545	550	555 560
Val Pro Ala Pro Phe Phe Leu Pro Ala Ser Leu Ser Ala Asn Asn Thr 565	570	575
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<210> 29

<211> 2472

<212> DNA

<213> Homo sapiens

<400> 29

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<210> 30

<211> 570

<212> PRT

<213> Homo sapiens

<400> 30

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Leu Thr Thr Glu Arg Val Arg Thr Thr Leu Ser Val Leu Lys Arg Ile
20          25          30

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Val Thr Ser Cys Tyr Gly Pro Ser Gly Arg Leu Lys Gln Leu His Asn
35          40          45

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Gly Phe Gly Gly Tyr Val Cys Thr Thr Ser Gln Ser Ser Ala Leu Leu
50          55          60

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Ser His Leu Leu Val Thr His Pro Ile Leu Lys Ile Leu Thr Ala Ser
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Ile Gln Asn His Val Ser Ser Phe Ser Asp Cys Gly Leu Phe Thr Ala
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 Glu Leu Lys Leu Thr Cys Gln Thr Ala Leu His Val Leu Gln Leu Thr
 385 390 395 400
 Leu Lys Glu Pro Trp Ala Leu Leu Gly Gly Gly Cys Thr Glu Thr His
 405 410 415

Leu Ala Ala Tyr Ile Arg His Lys Thr His Asn Asp Pro Glu Ser Ile
 420 425 430
 Leu Lys Asp Asp Glu Cys Thr Gln Thr Glu Leu Gln Leu Ile Ala Glu
 435 440 445
 Ala Phe Cys Ser Ala Leu Glu Ser Val Val Gly Ser Leu Glu His Asp
 450 455 460
 Gly Gly Glu Ile Leu Thr Asp Met Lys Tyr Gly His Leu Trp Ser Val
 465 470 475 480
 Gln Ala Asp Ser Pro Cys Val Ala Asn Trp Pro Asp Leu Leu Ser Gln
 485 490 495
 Cys Gly Cys Gly Leu Tyr Asn Ser Gln Glu Glu Leu Asn Trp Ser Phe
 500 505 510
 Leu Arg Ser Thr Arg Arg Pro Phe Val Pro Gln Ser Cys Leu Pro His
 515 520 525
 Glu Ala Val Gly Ser Ala Ser Asn Leu Thr Leu Asp Cys Leu Thr Ala
 530 535 540
 Lys Leu Ser Gly Leu Gln Val Ala Val Glu Thr Ala Asn Leu Ile Trp
 545 550 555 560
 Asp Leu Ser Tyr Val Ile Glu Asp Lys Asn
 565 570

<210> 31

<211> 1527

<212> DNA

<213> Homo sapiens

<400> 31

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<210> 32

<211> 315

<212> PRT

<213> Homo sapiens

<400> 32

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Asp Ala Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu Gly Met Lys
 35 40 45

Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln Met Trp Gln
 50 55 60

Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr Ala Asn Ile
 65 70 75 80

Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln Val Arg Ser
 85 90 95

Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn Phe Pro Gln
 100 105 110

Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val Phe Thr Leu
 115 120 125

Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr Ile Ile Arg
 130 135 140

Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe Gly Tyr Trp
 145 150 155 160

Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu Cys Asn Ala
 165 170 175

Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr Gly Leu Phe
 180 185 190

Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His Leu His Ala
 195 200 205

Leu Phe Tyr Leu Phe Trp Arg Leu Val Gly Gly Leu Ser Thr Leu Arg
 210 215 220

Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr Gln Arg Leu
 225 230 235 240

Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe Leu Leu Tyr
 245 250 255

Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu Asp Thr Leu

260 265 270
 Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg Asp Ile Pro
 275 280 285
 Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu Asn Ala Thr
 290 295 300
 Ala Lys Ala Val Ala Val Thr Leu Gln Ser His
 305 310 315

<210> 33
 <211> 988
 <212> DNA
 <213> Homo sapiens

<400> 33
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 gtccttcggc cttctccgtg tgttctccat tgtgatcccc tttctctatg tcgggacact 660
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<210> 34
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 34
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 20 25 30
 Ala Ala Trp Ser Gly Ser Gly Arg Ser Leu Val Pro Ser Arg Ser Val
 35 40 45
 Ile Val Thr Arg Ser Gly Ala Ile Leu Pro Lys Pro Val Lys Met Ser
 50 55 60
 Phe Gly Leu Leu Arg Val Phe Ser Ile Val Ile Pro Phe Leu Tyr Val
 65 70 75 80
 Gly Thr Leu Ile Ser Lys Asn Phe Ala Ala Leu Leu Glu Glu His Asp
 85 90 95

Ile Phe Val Pro Glu Asp Asp Asp Asp Asp
100 105

<210> 35
<211> 1759
<212> DNA
<213> Homo sapiens

<400> 35
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 catacaacgc tgaacttcca taacagtcaa tggtagagtc aaacatcaca tgtacagaac 180
 acacaattta gatgaactga aattataaga taaaataaaa taaaatccaa tttcagaaaa 240
 caaaaatcaa aacattaagg atccctgaaa tattcttaaa ccctaattgag atttcactgg 300
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 cagacatgcc ttgttgga caatgaaatc gatggagcac tgcacaccag aatgattggc 600
 caatgagcag cttctctccc tgaacaata actgccatt tggcaaaggg aaagatgaca 660
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<210> 36
<211> 87
<212> PRT
<213> Homo sapiens

<400> 36
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 Asn Leu Thr Val Gln Glu Leu Phe Leu Glu Leu Thr Pro Leu Leu Ser
 20 25 30
 Leu Met Cys Ile Pro Leu Cys Ala Phe Leu Tyr Asn His Ser Ser Phe
 35 40 45
 Asn Phe Pro Gly Glu Pro Ser Leu Ser Ala Ile Thr Thr Ser Phe Gln
 50 55 60
 Val Ser Ser Tyr Phe His His His Asn Gln Tyr Gly Ala Ile Ile Tyr

65

70

75

80

Leu Cys Thr Cys Ser Tyr Val

85

<210> 37

<211> 643

<212> DNA

<213> Homo sapiens

<400> 37

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 agttcagcca gtacgtgtgt cagcagacag gcctgcagat accccagctc ccagccccctc 360
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<210> 38

<211> 140

<212> PRT

<213> Homo sapiens

<400> 38

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 20 25 30
 Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr
 35 40 45
 Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln
 50 55 60
 Lys Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr
 65 70 75 80
 Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro
 85 90 95
 Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr
 100 105 110
 Val Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser
 115 120 125
 Lys Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys
 130 135 140

<210> 39

<211> 2015

<212> DNA

<213> Homo sapiens

<400> 39

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<210> 40

<211> 300

<212> PRT

<213> Homo sapiens

<400> 40

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Phe Phe Cys Pro Asn Glu Glu Ala Cys Pro Leu Lys Pro Ala Lys Gly
  20           25           30

Leu Met Ser Tyr Arg Ile Ile Thr Asp Phe Pro Ser Leu Thr Arg Asn
  35           40           45

Leu Pro Ser Gln Glu Leu Pro Gln Glu Asp Ser Leu Leu His Gly Gln
  50           55           60

Phe Ser Gln Ala Val Thr Pro Leu Ala His His His Thr Asp Tyr Ser
  65           70           75           80

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Lys Pro Thr Asp Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly
 85 90 95
 Ser Ser Asp His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala
 100 105 110
 Gln Leu Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe
 115 120 125
 Ser Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala
 130 135 140
 Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala Thr
 145 150 155 160
 Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr Pro Ser
 165 170 175
 Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro Val Thr Thr
 180 185 190
 Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr Val Phe Thr Arg
 195 200 205
 Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr Ala Val Leu Thr Thr
 210 215 220
 Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly Ser Leu Glu Thr Ile Pro
 225 230 235 240
 Phe Thr Glu Ile Ser Asn Leu Thr Leu Asn Thr Gly Asn Val Tyr Asn
 245 250 255
 Pro Thr Ala Leu Ser Met Ser Asn Val Glu Ser Ser Thr Met Asn Lys
 260 265 270
 Thr Ala Ser Trp Glu Gly Arg Glu Ala Ser Pro Gly Ser Ser Ser Pro
 275 280 285
 Gly Gln Cys Ser Arg Lys Ser Val Arg Pro Ser Ile
 290 295 300

<210> 41

<211> 1549

<212> DNA

<213> Homo sapiens

<400> 41

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<210> 42

<211> 396

<212> PRT

<213> Homo sapiens

<400> 42

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Phe Gly Leu Phe Ile Ile Phe Tyr Ser Ala Ile Ile Gly Gly Lys Ile
      20              25              30

Leu Gln Leu Ile Arg Ile Pro Leu Val Pro Pro Leu Pro Pro Leu Leu
      35              40              45

Gly Met Leu Leu Ala Gly Phe Thr Ile Arg Asn Val Pro Phe Ile Asn
      50              55              60

Glu His Val His Val Pro Asn Thr Trp Ser Ser Ile Leu Arg Ser Ile
      65              70              75              80

Ala Leu Thr Ile Ile Leu Ile Arg Ala Gly Leu Gly Leu Asp Pro Gln
      85              90              95

Ala Leu Arg His Leu Lys Val Val Cys Phe Arg Leu Ala Val Gly Pro
      100             105             110

Cys Leu Met Glu Ala Ser Ala Ala Ala Val Phe Ser His Phe Ile Met
      115             120             125

Lys Phe Pro Trp Gln Trp Ala Phe Leu Leu Gly Phe Val Leu Gly Ala
      130             135             140

Val Ser Pro Ala Val Val Val Pro Tyr Met Met Val Leu Gln Glu Asn
      145             150             155             160

Gly Tyr Gly Val Glu Glu Gly Ile Pro Thr Leu Leu Met Ala Ala Ser
      165             170             175

Ser Met Asp Asp Ile Leu Ala Ile Thr Gly Phe Asn Thr Cys Leu Ser
      180             185             190

Ile Val Phe Ser Ser Gly Gly Ile Leu Asn Asn Ala Ile Ala Ser Ile
      195             200             205

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Arg Asn Val Cys Ile Ser Leu Leu Ala Gly Ile Val Leu Gly Phe Phe
 210 215 220
 Val Arg Tyr Phe Pro Ser Glu Asp Gln Lys Lys Leu Thr Leu Lys Arg
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 Gly Phe Leu Val Leu Thr Met Cys Val Ser Ala Val Leu Gly Ser Gln
 245 250 255
 Arg Ile Gly Leu His Gly Ser Gly Gly Leu Cys Thr Leu Val Leu Ser
 260 265 270
 Phe Ile Ala Gly Thr Lys Trp Ser Gln Glu Lys Met Lys Val Gln Lys
 275 280 285
 Ile Ile Thr Thr Val Trp Asp Ile Phe Gln Pro Leu Leu Phe Gly Leu
 290 295 300
 Val Gly Ala Glu Val Ser Val Ser Ser Leu Glu Ser Asn Ile Val Gly
 305 310 315 320
 Ile Ser Val Ala Thr Leu Ser Leu Ala Leu Cys Val Arg Ile Leu Thr
 325 330 335
 Thr Tyr Leu Leu Met Cys Phe Ala Gly Phe Ser Phe Lys Glu Lys Ile
 340 345 350
 Phe Ile Ala Leu Ala Trp Met Pro Lys Ala Thr Val Gln Ile Asn Gln
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 385 390 395

<210> 43
 <211> 4433
 <212> DNA
 <213> Homo sapiens

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<211> 439

<212> PRT

<213> Homo sapiens

<400> 44

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Ser Leu Leu Gly Ser Ala Ala Glu Pro Ala Arg Gly Pro Pro Pro Gln
      35             40             45

His Pro Leu Gln Gly Arg Lys Glu Lys Arg Val Asp Asn Ile Glu Ile
      50             55             60

Gln Lys Phe Ile Ser Lys Lys Ala Asp Leu Leu Phe Ala Leu Ser Trp
      65             70             75             80

Lys Ser Asp Ala Pro Ala Thr Ser Glu Ile Asn Glu Asp Ser Glu Asp
      85             90             95

His Tyr Ala Ile Met Pro Pro Leu Glu Gln Phe Met Glu Ile Pro Ser
      100            105            110

Met Asp Arg Arg Glu Leu Phe Phe Arg Asp Ile Glu Arg Gly Asp Ile
      115            120            125

Val Ile Gly Arg Ile Ser Ser Ile Arg Glu Phe Gly Phe Phe Met Val
      130            135            140

Leu Ile Cys Leu Gly Ser Gly Ile Met Arg Asp Ile Ala His Leu Glu
      145            150            155            160

Ile Thr Ala Leu Cys Pro Leu Arg Asp Val Pro Ser His Ser Asn His
      165            170            175

Gly Asp Pro Leu Ser Tyr Tyr Gln Thr Gly Asp Ile Ile Arg Ala Gly
      180            185            190

Ile Lys Asp Ile Asp Arg Tyr His Glu Lys Leu Ala Val Ser Leu Tyr
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Ser Ser Ser Leu Pro Pro His Leu Ser Gly Ile Lys Leu Gly Val Ile
      210            215            220

Ser Ser Glu Glu Leu Pro Leu Tyr Tyr Arg Arg Ser Val Glu Leu Asn
      225            230            235            240

Ser Asn Ser Leu Glu Ser Tyr Glu Asn Val Met Gln Ser Ser Leu Gly
      245            250            255

Phe Val Asn Pro Gly Val Val Glu Phe Leu Leu Glu Lys Leu Gly Ile
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Asp Glu Ser Asn Pro Pro Ser Leu Met Arg Gly Leu Gln Ser Lys Asn
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Phe Ser Glu Asp Asp Phe Ala Ser Ala Leu Arg Lys Lys Gln Ser Ala

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 Glu Asn Cys Pro Thr His Arg Asn Ala Arg Lys Tyr Leu Cys Gln Thr
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<210> 45

<211> 4017

<212> DNA

<213> Homo sapiens

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<210> 46

<211> 1152

<212> PRT

<213> Homo sapiens

<400> 46

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Met Phe Glu Lys Ile His Gln Glu Thr Phe Gly Lys Ser Gly Cys Ser
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Arg Ile Val Pro Gly Gln Phe Leu Ala Val Asp Pro Lys Gly Arg Ala

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Lys Ala Asn Thr Leu Val Tyr His Val Val Gly Val Asp Val Gly Phe		
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Glu Asn Pro Met Phe Ala Cys Leu Glu Met Asp Tyr Glu Glu Ala Asp		
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Asn Asp Pro Thr Gly Glu Ala Ala Ala Asn Thr Gln Gln Thr Leu Thr		
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Phe Tyr Glu Leu Asp Leu Gly Leu Asn His Val Val Arg Lys Tyr Ser		
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Glu Pro Leu Glu Glu His Gly Asn Phe Leu Ile Thr Val Pro Gly Gly		
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Ser Asp Gly Pro Ser Gly Val Leu Ile Cys Ser Glu Asn Tyr Ile Thr		
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Tyr Lys Asn Phe Gly Asp Gln Pro Asp Ile Arg Cys Pro Ile Pro Arg		
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Glu Gln Gly Asp Ile Phe Lys Ile Thr Leu Glu Thr Asp Glu Asp Met		
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Val Thr Glu Ile Arg Leu Lys Tyr Phe Asp Thr Val Pro Val Ala Ala		
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Glu Pro Glu Phe Ser Ser Ala Met Pro Leu Glu Glu Gly Asp Thr Phe		
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	325	330 335
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	340	345 350
Glu Asp Thr Pro Gln Leu Tyr Val Ala Cys Gly Arg Gly Pro Arg Ser		
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Ser Leu Arg Val Leu Arg His Gly Leu Glu Val Ser Glu Met Ala Val		

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Ser Tyr Ser Tyr Gln Ser Arg Phe His Leu Thr Pro Leu Ser Tyr Glu 660 665 670		
Thr Leu Glu Phe Ala Ser Gly Phe Ala Ser Glu Gln Cys Pro Glu Gly 675 680 685		
Ile Val Ala Ile Ser Thr Asn Thr Leu Arg Ile Leu Ala Leu Glu Lys		

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Arg Lys Phe Val Ile His Pro Glu Ser Asn Asn Leu Ile Ile Ile Glu 725	730	735
Thr Asp His Asn Ala Tyr Thr Glu Ala Thr Lys Ala Gln Arg Lys Gln 740	745	750
Gln Met Ala Glu Glu Met Val Glu Ala Ala Gly Glu Asp Glu Arg Glu 755	760	765
Leu Ala Ala Glu Met Ala Ala Ala Phe Leu Asn Glu Asn Leu Pro Glu 770	775	780
Ser Ile Phe Gly Ala Pro Lys Ala Gly Asn Gly Gln Trp Ala Ser Val 785	790	795 800
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Asn Thr Gly Glu Asp Trp Tyr Val Leu Val Gly Val Ala Lys Asp Leu 835	840	845
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Gln Thr Ile Gly His Arg Val Ile Val Ser Asp Val Gln Glu Ser Phe 930	935	940
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Lys Ala Leu Trp Asp Arg Gly Leu Leu Asn Gly Ala Ser Gln Lys Ala		

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<210> 47

<211> 2635

<212> DNA

<213> Homo sapiens

<400> 47

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<211> 97

<212> PRT

<213> Homo sapiens

<400> 48

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Phe Pro Met Val Ser Gly Tyr Phe Leu Gly Phe Pro Tyr Ser Ser Phe
 20 25 30

Ile Ser Phe Phe Phe Ile Phe Ala Phe Leu Ser Thr Ala Phe Arg Phe
 35 40 45

Ala Gly Asp Ala Ser Phe Ser Ser Met Phe Gly Phe Ser Gln Tyr Gly
 50 55 60

Asn Phe Arg Arg Thr Glu Glu Arg Arg Glu Glu Glu Glu Ser Ile Leu
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Leu Gln Asn Phe Ser Asp Leu Leu Trp Gln Ser Ser Gly Arg Lys Val
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Phe

<210> 49

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 49

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<210> 50

<211> 141

<212> PRT

<213> Homo sapiens

<400> 50

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Met Ser Phe Ser Leu Asn Phe Thr Leu Pro Ala Asn Thr Thr Ser Ser
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Pro Val Thr Gly Gly Lys Glu Thr Asp Cys Gly Pro Ser Leu Gly Leu
          20             25             30

Ala Ala Gly Ile Pro Leu Leu Val Ala Thr Ala Leu Leu Val Ala Leu
      35             40             45

Leu Phe Thr Leu Ile His Pro Arg Arg Ser Ser Ile Glu Ala Met Glu
 50             55             60

Glu Ser Asp Arg Pro Cys Glu Ile Ser Glu Ile Asp Asp Asn Pro Lys
 65             70             75             80

Ile Ser Glu Asn Pro Arg Arg Ser Pro Thr His Glu Lys Asn Thr Met
          85             90             95

Gly Ala Gln Glu Ala His Ile Tyr Val Lys Thr Val Ala Gly Ser Glu
      100             105             110

Glu Pro Val His Asp Arg Tyr Arg Pro Thr Ile Glu Met Glu Arg Arg
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Arg Gly Leu Trp Trp Leu Val Pro Arg Leu Ser Leu Glu
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<210> 51

<211> 5160

<212> DNA

<213> Homo sapiens

<400> 51

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<210> 52

<211> 1135

<212> PRT

<213> Homo sapiens

<400> 52

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Met His Gln Met Asn Ala Lys Met His Phe Arg Phe Val Phe Ala Leu
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Leu Ile Val Ser Phe Asn His Asp Val Leu Gly Lys Asn Leu Lys Tyr
      20              25              30

```

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Arg Ile Tyr Glu Glu Gln Arg Val Gly Ser Val Ile Ala Arg Leu Ser
      35              40              45

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Glu Asp Val Ala Asp Val Leu Leu Lys Leu Pro Asn Pro Ser Thr Val
      50              55              60

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Arg Phe Arg Ala Met Gln Arg Gly Asn Ser Pro Leu Leu Val Val Asn
      65              70              75              80

```

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Glu Asp Asn Gly Glu Ile Ser Ile Gly Ala Thr Ile Asp Arg Glu Gln
      85              90              95

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Leu Cys Gln Lys Asn Leu Asn Cys Ser Ile Glu Phe Asp Val Ile Thr
      100             105             110

```

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Leu Pro Thr Glu His Leu Gln Leu Phe His Ile Glu Val Glu Val Leu
      115             120             125

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Asp Ile Asn Asp Asn Ser Pro Gln Phe Ser Arg Ser Leu Ile Pro Ile
      130             135             140

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WO 00/09552

PCT/US99/18298

Glu Ile Ser Glu Ser Ala Ala Val Gly Thr Arg Ile Pro Leu Asp Ser
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Ala Phe Asp Pro Asp Val Gly Glu Asn Ser Leu His Thr Tyr Ser Leu
165 170 175

Ser Ala Asn Asp Phe Phe Asn Ile Glu Val Arg Thr Arg Thr Asp Gly
180 185 190

Ala Lys Tyr Ala Glu Leu Ile Val Val Arg Glu Leu Asp Arg Glu Leu
195 200 205

Lys Ser Ser Tyr Glu Leu Gln Leu Thr Ala Ser Asp Met Gly Val Pro
210 215 220

Gln Arg Ser Gly Ser Ser Ile Leu Lys Ile Ser Ile Ser Asp Ser Asn
225 230 235 240

Asp Asn Ser Pro Ala Phe Glu Gln Gln Ser Tyr Ile Ile Gln Leu Leu
245 250 255

Glu Asn Ser Pro Val Gly Thr Leu Leu Leu Asp Leu Asn Ala Thr Asp
260 265 270

Pro Asp Glu Gly Ala Asn Gly Lys Ile Val Tyr Ser Phe Ser Ser His
275 280 285

Val Ser Pro Lys Ile Met Glu Thr Phe Lys Ile Asp Ser Glu Arg Gly
290 295 300

His Leu Thr Leu Phe Lys Gln Val Asp Tyr Glu Ile Thr Lys Ser Tyr
305 310 315 320

Glu Ile Asp Val Gln Ala Gln Asp Leu Gly Pro Asn Ser Ile Pro Ala
325 330 335

His Cys Lys Ile Ile Ile Lys Val Val Asp Val Asn Asp Asn Lys Pro
340 345 350

Glu Ile Asn Ile Asn Leu Met Ser Pro Gly Lys Glu Glu Ile Ser Tyr
355 360 365

Ile Phe Glu Gly Asp Pro Ile Asp Thr Phe Val Ala Leu Val Arg Val
370 375 380

Gln Asp Lys Asp Ser Gly Leu Asn Gly Glu Ile Val Cys Lys Leu His
385 390 395 400

Gly His Gly His Phe Lys Leu Gln Lys Thr Tyr Glu Asn Asn Tyr Leu
405 410 415

Ile Leu Thr Asn Ala Thr Leu Asp Arg Glu Lys Arg Ser Glu Tyr Ser
420 425 430

Leu Thr Val Ile Ala Glu Asp Arg Gly Thr Pro Ser Leu Ser Thr Val
435 440 445

Lys His Phe Thr Val Gln Ile Asn Asp Ile Asn Asp Asn Pro Pro His
450 455 460

WO 00/09552

PCT/US99/18298

Phe Gln Arg Ser Arg Tyr Glu Phe Val Ile Ser Glu Asn Asn Ser Pro
 465 470 475 480

Gly Ala Tyr Ile Thr Thr Val Thr Ala Thr Asp Pro Asp Leu Gly Glu
 485 490 495

Asn Gly Gln Val Thr Tyr Thr Ile Leu Glu Ser Phe Ile Leu Gly Ser
 500 505 510

Ser Ile Thr Thr Tyr Val Thr Ile Asp Pro Ser Asn Gly Ala Ile Tyr
 515 520 525

Ala Leu Arg Ile Phe Asp His Glu Glu Val Ser Gln Ile Thr Phe Val
 530 535 540

Val Glu Ala Arg Asp Gly Gly Ser Pro Lys Gln Leu Val Ser Asn Thr
 545 550 555 560

Thr Val Val Leu Thr Ile Ile Asp Glu Asn Asp Asn Val Pro Val Val
 565 570 575

Ile Gly Pro Ala Leu Arg Asn Asn Thr Ala Glu Ile Thr Ile Pro Lys
 580 585 590

Gly Ala Glu Ser Gly Phe His Val Thr Arg Ile Arg Ala Ile Asp Arg
 595 600 605

Asp Ser Gly Val Asn Ala Glu Leu Ser Cys Ala Ile Val Ala Gly Asn
 610 615 620

Glu Glu Asn Ile Phe Ile Ile Asp Pro Arg Ser Cys Asp Ile His Thr
 625 630 635 640

Asn Val Ser Met Asp Ser Val Pro Tyr Thr Glu Trp Glu Leu Ser Val
 645 650 655

Ile Ile Gln Asp Lys Gly Asn Pro Gln Leu His Thr Lys Val Leu Leu
 660 665 670

Lys Cys Met Ile Phe Glu Tyr Ala Glu Ser Val Thr Ser Thr Ala Met
 675 680 685

Thr Ser Val Ser Gln Ala Ser Leu Asp Val Ser Met Ile Ile Ile Ile
 690 695 700

Ser Leu Gly Ala Ile Cys Ala Val Leu Leu Val Ile Met Val Leu Phe
 705 710 715 720

Ala Thr Arg Cys Asn Arg Glu Lys Lys Asp Thr Arg Ser Tyr Asn Cys
 725 730 735

Arg Val Ala Glu Ser Thr Tyr Gln His His Pro Lys Arg Pro Ser Arg
 740 745 750

Gln Ile His Lys Gly Asp Ile Thr Leu Val Pro Thr Ile Asn Gly Thr
 755 760 765

Leu Pro Ile Arg Ser His His Arg Ser Ser Pro Ser Ser Ser Pro Thr
 770 775 780

Leu Glu Arg Gly Gln Met Gly Ser Arg Gln Ser His Asn Ser His Gln
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 Met Asp Lys Phe Ser Leu Lys Asp Ser Gly Arg Gly Asp Ser Glu Ala
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 Asp Glu Asp Thr Gly Asp Thr Ser Ser Ser Leu Leu Ser Glu Met
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 Pro Leu Pro Ala Lys Thr Val Gly Tyr Pro Gln Gly Val Ala Ala Trp
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 Leu Gly Thr His Ser Ser Val Gln Pro Ser Ser Lys Trp Leu Pro Ala
 1075 1080 1085
 Met Glu Glu Ile Pro Glu Asn Tyr Glu Glu Asp Asp Phe Asp Asn Val
 1090 1095 1100

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<211> 208

<212> PRT

<213> Homo sapiens

<400> 56

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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 58

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Lys	Val	Arg	Arg	Ser	Thr	Ser	Arg	Asp	Arg	Leu	Asp	Asp	Ile	Ile	Val	50	55	60	
Leu	Thr	Lys	Asp	Ile	Gln	Glu	Gly	Asp	Thr	Leu	Asn	Ala	Ile	Ala	Leu	65	70	75	80
Gln	Tyr	Cys	Cys	Thr	Val	Ala	Asp	Ile	Lys	Arg	Val	Asn	Asn	Leu	Ile	85	90	95	
Ser	Asp	Gln	Asp	Phe	Phe	Ala	Leu	Arg	Ser	Ile	Lys	Ile	Pro	Val	Lys	100	105	110	
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<212> DNA

<213> Homo sapiens

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<210> 60

<211> 568

<212> PRT

<213> Homo sapiens

<400> 60

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Met Lys Ser Asp Ser Phe Ala Pro Lys Thr Asp Ser Glu Lys Pro Phe
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Arg Gly Ser Gln Ser Pro Lys Arg Tyr Lys Leu Arg Asp Asp Phe Glu
  20          25          30

Lys Lys Met Ala Asp Phe His Lys Glu Glu Met Asp Asp Gln Asp Lys
  35          40          45

Asp Lys Ala Lys Gly Arg Lys Glu Ser Glu Phe Asp Asp Glu Pro Lys
  50          55          60

Phe Met Ser Lys Val Ile Gly Ala Asn Lys Asn Gln Glu Glu Glu Lys
  65          70          75          80

Ser Gly Lys Trp Glu Gly Leu Val Tyr Ala Pro Pro Gly Lys Glu Lys
  85          90          95

Gln Arg Lys Thr Glu Glu Leu Glu Glu Glu Ser Phe Pro Glu Arg Ser
 100         105         110

Lys Lys Glu Asp Arg Gly Lys Arg Ser Glu Gly Gly His Arg Gly Phe
 115         120         125

Val Pro Glu Lys Asn Phe Arg Val Thr Ala Tyr Lys Ala Val Gln Glu
 130         135         140

Lys Ser Ser Ser Pro Pro Pro Arg Lys Thr Ser Glu Ser Arg Asp Lys
 145         150         155         160

Leu Gly Ala Lys Gly Asp Phe Pro Thr Gly Lys Ser Ser Phe Ser Ile
 165         170         175

Thr Arg Glu Ala Gln Val Asn Val Arg Met Asp Ser Phe Asp Glu Asp
 180         185         190

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Leu Ala Arg Pro Ser Gly Leu Leu Ala Gln Glu Arg Lys Leu Cys Arg
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 Asp Leu Val His Ser Asn Lys Lys Glu Gln Glu Phe Arg Ser Ile Phe
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 Gln His Ile Gln Ser Ala Gln Ser Gln Arg Ser Pro Ser Glu Leu Phe
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 Ala Gln His Ile Val Thr Ile Val His His Val Lys Glu His His Phe
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 Gly Ser Ser Gly Met Thr Leu His Glu Arg Phe Thr Lys Tyr Leu Lys
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 Arg Gly Thr Glu Gln Glu Ala Ala Lys Asn Lys Lys Ser Pro Glu Ile
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 His Arg Arg Ile Asp Ile Ser Pro Ser Thr Phe Arg Lys His Gly Leu
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 Ala His Asp Glu Met Lys Ser Pro Arg Glu Pro Gly Tyr Lys Ala Glu
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 Gly Lys Tyr Lys Asp Asp Pro Val Asp Leu Arg Leu Asp Ile Glu Arg
 325 330 335
 Arg Lys Lys His Lys Glu Arg Asp Leu Lys Arg Gly Lys Ser Arg Glu
 340 345 350
 Ser Val Asp Ser Arg Asp Ser Ser His Ser Arg Glu Arg Ser Ala Glu
 355 360 365
 Lys Thr Glu Lys Thr His Lys Gly Ser Lys Lys Gln Lys Lys His Pro
 370 375 380
 Arg Ala Arg Asp Arg Ser Arg Ser Ser Ser Ser Ser Gln Ser Ser
 385 390 395 400
 His Ser Tyr Lys Ala Glu Glu Tyr Thr Glu Glu Thr Glu Glu Arg Glu
 405 410 415
 Glu Ser Thr Thr Gly Phe Asp Lys Ser Arg Leu Gly Thr Lys Asp Phe
 420 425 430
 Val Gly Pro Ser Glu Arg Gly Gly Gly Arg Ala Arg Gly Thr Phe Gln
 435 440 445
 Phe Arg Ala Arg Gly Arg Gly Trp Gly Arg Gly Asn Tyr Ser Gly Asn
 450 455 460
 Asn Asn Asn Asn Ser Asn Asn Asp Phe Gln Lys Arg Asn Arg Glu Glu
 465 470 475 480
 Glu Trp Asp Pro Glu Tyr Thr Pro Lys Ser Lys Lys Tyr Asn Leu His
 485 490 495
 Asp Asp Arg Glu Gly Glu Gly Ser Asp Lys Trp Val Ser Arg Gly Arg
 500 505 510

Gly Arg Gly Ala Phe Pro Arg Gly Arg Gly Arg Phe Met Phe Arg Lys
515 520 525

Ser Ser Thr Ser Pro Lys Trp Ala His Asp Lys Phe Ser Gly Glu Glu
530 535 540

Gly Glu Ile Glu Asp Asp Glu Ser Gly Thr Glu Asn Arg Glu Glu Lys
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Asp Asn Ile Gln Pro Thr Thr Glu
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<210> 61

<211> 3145

<212> DNA

<213> Homo sapiens

<400> 61

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<210> 62

<211> 574

<212> PRT

<213> Homo sapiens

<400> 62

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Pro Arg Cys Ser Arg Lys Ala Ala Gly Thr Lys Gln Thr Ser Thr Leu
          20              25              30

Lys Gln Glu Asp Ala Ser Lys Arg Gly Gly Ser Leu Arg Pro Ala His
          35              40              45

Tyr Ser Asp Val Val Asp Glu Arg Ser Ile Val Lys Leu Cys Gly Tyr
          50              55              60

Pro Leu Cys Gln Lys Lys Leu Gly Ile Val Pro Lys Gln Lys Tyr Lys
          65              70              75              80

Ile Ser Thr Lys Thr Asn Lys Val Tyr Asp Ile Thr Glu Arg Lys Ser
          85              90              95

Ile Ser Thr Lys Thr Asn Lys Val Tyr Asp Ile Thr Glu Arg Lys Ser
          85              90              95

Phe Cys Ser Asn Phe Cys Tyr Gln Ala Ser Lys Phe Phe Glu Ala Gln
          100             105             110

Ile Pro Lys Thr Pro Val Trp Val Arg Glu Glu Glu Arg His Pro Asp
          115             120             125

Phe Gln Leu Leu Lys Glu Glu Gln Ser Gly His Ser Gly Glu Glu Val
          130             135             140

Gln Leu Cys Ser Lys Ala Ile Lys Thr Ser Asp Ile Asp Asn Pro Ser
          145             150             155             160

His Phe Glu Lys Gln Tyr Glu Ser Ser Ser Ser Thr His Ser Asp
          165             170             175

Ser Ser Ser Asp Asn Glu Gln Asp Phe Val Ser Ser Ile Leu Pro Gly
          180             185             190

Asn Arg Pro Asn Ser Thr Asn Ile Arg Pro Gln Leu His Gln Lys Ser
          195             200             205

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Ile Met Lys Lys Lys Ala Gly His Lys Ala Asn Ser Lys His Lys His
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 245 250 255
 Val Asn Thr Gln Ser Ser Ser Asn Ser Thr Leu Pro Glu Arg Leu Lys
 260 265 270
 Ala Ser Glu Asn Ser Glu Ser Glu Tyr Ser Arg Ser Glu Ile Thr Leu
 275 280 285
 Val Gly Ile Ser Lys Lys Ser Ala Glu His Phe Lys Arg Lys Phe Ala
 290 295 300
 Lys Ser Asn Gln Val Ser Arg Ser Val Ser Asn Ser Val Gln Val Cys
 305 310 315 320
 Pro Glu Val Gly Lys Arg Asn Leu Leu Lys Val Leu Lys Glu Thr Leu
 325 330 335
 Ile Glu Trp Lys Thr Glu Glu Thr Leu Arg Phe Leu Tyr Gly Gln Asn
 340 345 350
 Tyr Ala Ser Val Cys Leu Lys Pro Glu Ala Ser Leu Val Lys Glu Glu
 355 360 365
 Leu Asp Glu Asp Asp Ile Ile Ser Asp Pro Asp Ser Pro Phe Pro Ala
 370 375 380
 Trp Arg Glu Ser Gln Asn Ser Leu Asp Glu Ser Leu Pro Phe Arg Gly
 385 390 395 400
 Ser Gly Thr Ala Ile Lys Pro Leu Pro Ser Tyr Glu Asn Leu Lys Lys
 405 410 415
 Glu Thr Glu Lys Leu Asn Leu Arg Ile Arg Glu Phe Tyr Arg Gly Arg
 420 425 430
 Tyr Val Leu Gly Glu Glu Thr Thr Lys Ser Gln Asp Ser Glu Glu His
 435 440 445
 Asp Ser Thr Phe Pro Leu Ile Asp Ser Ser Ser Gln Asn Gln Ile Arg
 450 455 460
 Lys Arg Ile Val Leu Glu Lys Leu Ser Lys Val Leu Pro Gly Leu Leu
 465 470 475 480
 Val Pro Leu Gln Ile Thr Leu Gly Asp Ile Tyr Thr Gln Leu Lys Asn
 485 490 495
 Leu Val Arg Thr Phe Arg Leu Thr Asn Arg Asn Ile Ile His Lys Pro
 500 505 510
 Ala Glu Trp Thr Leu Ile Ala Met Val Leu Leu Ser Leu Leu Thr Pro
 515 520 525

Ile Leu Gly Ile Gln Lys His Ser Gln Glu Gly Met Val Phe Thr Arg
530 535 540

Phe Leu Asp Thr Leu Leu Glu Glu Leu His Leu Lys Asn Glu Asp Leu
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Glu Ser Leu Thr Ile Ile Phe Arg Thr Ser Cys Leu Pro Glu
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<211> 1812
<212> DNA
<213> Homo sapiens

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<211> 98
<212> PRT
<213> Homo sapiens

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20 25 30

Ser Ile Phe Phe Phe Phe Leu Ser Pro Asn Leu Asn Arg Ser Lys Met
 35 40 45

Cys Ser Gly Ile Pro Gly Asn Arg Cys Val Cys Lys Val Lys Asn Arg
 50 55 60

Leu Phe Arg Asn Ser Leu Phe Arg Tyr Leu His Pro Ala Ser His Val
 65 70 75 80

Lys Tyr Leu Ser Leu Lys Gly Leu Arg Cys Thr Ser Phe Ile Ser Tyr
 85 90 95

Phe Ser

<210> 65
 <211> 1558
 <212> DNA
 <213> Homo sapiens

<400> 65
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<210> 66
 <211> 437
 <212> PRT
 <213> Homo sapiens

<400> 66
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Val Val Ala Glu Thr Ser Gln Gly Ser Trp Ser Ala Pro His Phe Pro

20	25	30
Ile Tyr Leu Leu Ser Ser Pro 35	Pro Thr Pro Pro Pro 40	Pro Trp Leu Pro 45
Ser Leu Met Thr Ala Trp 50	Ile Leu Leu Pro Val 55	Ser Leu Ser Ala Phe 60
Ser Ile Thr Gly Ile Trp 65	Thr Val Tyr Ala Met 70	Ala Val Met Asn His 75 80
His Val Cys Pro Val Glu 85	Asn Trp Ser Tyr Asn 90	Glu Ser Cys Pro Pro 95
Asp Pro Ala Glu Gln Gly 100	Gly Pro Lys Thr Cys 105	Cys Thr Leu Asp Asp 110
Val Pro Leu Ile Ser Lys 115	Cys Gly Ser Tyr Pro 120	Pro Glu Ser Cys Leu 125
Phe Ser Leu Ile Gly Asn 130	Met Gly Ala Phe Met 135	Val Ala Leu Ile Cys 140
Leu Leu Arg Tyr Gly Gln 145	Leu Leu Glu Gln Ser 150	Arg His Ser Trp Val 155 160
Asn Thr Thr Ala Leu Ile 165	Thr Gly Cys Thr Asn 170	Ala Ala Gly Leu Leu 175
Val Val Gly Asn Phe Gln 180	Val Asp His Ala Arg 185	Ser Leu His Tyr Val 190
Gly Ala Gly Val Ala Phe 195	Pro Ala Gly Leu Leu 200	Phe Val Cys Leu His 205
Cys Leu Ser Pro Thr Lys 210	Gly Pro Pro Pro Arg 215	Trp Thr Trp Leu Trp 220
Pro Ile Cys Glu Val Cys 225	Trp Leu Ser Ser Pro 230	Leu Ser Pro Trp Ser 235 240
Ser Val Glu Ser Ser Leu 245	Ser Met Arg Val Leu 250	Ser Cys Asn Met Gly 255
Gln Pro Cys Val Ser Gly 260	Cys Val Ser Ser Ile 265	Ser Ser Phe Ser Met 270
Ala Pro Ser Ala Thr Ser 275	Leu Gly Gln Ser Pro 280	Gln Thr His Trp Trp 285
Leu His Cys Ser Leu Pro 290	Leu Ala Gly Pro Ala 295	Ser Pro Pro Gly Ala 300
Ala Ala Leu His Pro Pro 305	Gln Leu Cys Pro Arg 310	Glu His Arg Tyr Asp 315 320
Leu Arg Ser Gly Glu Gly 325	Gly Trp Pro Gly Ser 330	Thr Ala Pro His Pro 335
Ile Ser Ser Phe His Leu 340	Phe Arg Thr Lys Asn 345	Asn Phe Glu Lys Val 350

340 345 350
 Phe Cys Trp Asp Leu Gly Phe Leu Thr Ser Gly Glu Val Ala Ile Pro
 355 360 365
 Cys Pro Pro Val Pro Trp Arg Ser Gly Pro Cys Gln Leu Pro Gln Leu
 370 375 380
 His Asp Leu Leu Pro Thr Pro Arg Cys Arg Phe Val Phe Lys Gly His
 385 390 395 400
 Leu Ser Ser Leu Thr Gln Pro Ala Leu Gln Val Pro Ser Thr Pro Ser
 405 410 415
 Ala Lys Ala Arg Pro Leu Gly Phe Pro Ala Ala Gly Ile Gly Gly Trp
 420 425 430
 Glu Gln Gln Arg Gly
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<210> 67
 <211> 2336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (418)

<400> 67
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<210> 68

<211> 473

<212> PRT

<213> Homo sapiens

<400> 68

```

Met Met His Phe Lys Ser Gly Leu Glu Leu Thr Glu Leu Gln Asn Met
  1              5              10              15

```

```

Thr Val Pro Glu Asp Asp Asn Ile Ser Asn Asp Ser Asn Asp Phe Thr
          20              25              30

```

```

Glu Val Glu Asn Gly Gln Ile Asn Ser Lys Phe Ile Ser Asp Arg Glu
  35              40              45

```

```

Ser Arg Arg Ser Leu Thr Asn Ser His Leu Glu Lys Lys Lys Cys Asp
  50              55              60

```

```

Glu Tyr Ile Pro Gly Thr Thr Ser Leu Gly Met Phe Val Phe Asn Leu
  65              70              75              80

```

```

Ser Asn Ser Met Met Gly Ser Gly Ile Trp Asp Ser Leu Cys Pro Gly
          85              90              95

```

```

Asn Thr Gly Ile Leu Leu Phe Leu Val Leu Leu Thr Ser Val Thr Leu
  100              105              110

```

```

Leu Ser Ile Tyr Ser Ile Asn Leu Leu Leu Ile Cys Ser Lys Glu Thr
  115              120              125

```

```

Gly Cys Met Val Tyr Glu Lys Leu Gly Glu Gln Val Phe Gly Thr Thr
  130              135              140

```

```

Gly Lys Phe Val Ile Phe Gly Ala Thr Ser Leu Gln Asn Thr Gly Ala
  145              150              155              160

```

```

Met Leu Ser Tyr Leu Phe Ile Val Lys Asn Glu Leu Pro Ser Ala Ile
          165              170              175

```

```

Lys Phe Leu Met Gly Lys Glu Glu Thr Phe Ser Ala Trp Tyr Val Asp
          180              185              190

```

```

Gly Arg Val Leu Val Val Ile Val Thr Phe Gly Ile Ile Leu Pro Leu
          195              200              205

```

```

Cys Leu Leu Lys Asn Leu Gly Tyr Leu Gly Tyr Thr Ser Gly Phe Ser
  210              215              220

```

```

Leu Ser Cys Met Val Phe Phe Leu Ile Val Val Ile Tyr Lys Lys Phe

```


225 230 235 240
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 245 250 255
 Ser Thr Asn Ala Asp Thr Cys Thr Pro Lys Tyr Val Thr Phe Asn Ser
 260 265 270
 Lys Thr Val Tyr Ala Leu Pro Thr Ile Ala Cys Ala Phe Val Cys His
 275 280 285
 Pro Ser Val Leu Pro Ile Tyr Ser Glu Leu Lys Asp Arg Ser Gln Lys
 290 295 300
 Lys Met Gln Met Val Ser Asn Ile Ser Phe Phe Ala Met Phe Val Met
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 Tyr Phe Leu Thr Ala Ile Phe Gly Tyr Leu Thr Phe Tyr Asp Asn Val
 325 330 335
 Gln Ser Asp Leu Leu His Lys Tyr Gln Ser Lys Asp Asp Ile Leu Ile
 340 345 350
 Leu Thr Val Arg Leu Ala Val Ile Val Ala Val Ile Leu Thr Val Pro
 355 360 365
 Val Leu Phe Phe Thr Val Arg Ser Ser Leu Phe Glu Leu Ala Lys Lys
 370 375 380
 Thr Lys Phe Asn Leu Cys Arg His Thr Val Val Thr Cys Ile Leu Leu
 385 390 395 400
 Val Val Ile Asn Leu Leu Val Ile Phe Ile Pro Ser Met Lys Asp Ile
 405 410 415
 Phe Gly Val Val Gly Val Thr Ser Ala Asn Met Leu Ile Phe Ile Leu
 420 425 430
 Pro Ser Ser Leu Tyr Leu Lys Ile Thr Asp Gln Asp Gly Asp Lys Gly
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 Thr Gln Arg Ile Trp Val Cys Leu Leu Pro Ala Thr Leu Thr Phe Leu
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 Ile Ser Phe Pro Phe Lys Phe Thr Lys
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<210> 69

<211> 1999

<212> DNA

<213> Homo sapiens

<400> 69

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 aaaaattttt tttttagaaa atgggggtct tccaatgttg cccatgctgg tcttgaactc 240
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```

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```

<210> 70

<211> 153

<212> PRT

<213> Homo sapiens

<400> 70

```

Met Asn Cys Ser Phe Ala Val Arg Lys Thr Leu Thr Lys Arg Gln Lys
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```

```

Lys Phe His Ser Ile Ile Phe His Val Ser Ser Gly Leu Lys Ser Phe
      20                      25                      30

```

```

Ala Asn Lys Met Phe Ile Gly Trp Ser Gln Leu Thr Met Tyr Tyr Trp
      35                      40                      45

```

```

Gln His Phe Leu Asp Gly Tyr Leu Leu Gly Pro Phe Ile Arg Lys Arg
      50                      55                      60

```

```

Glu Arg Met Gly Trp Phe Cys Met Gly Ser Cys Leu Gly Val Lys Ile
      65                      70                      75                      80

```

```

Ala Glu Ser Val Ala Glu Asp Asn Asp Leu Pro Tyr Asn Ile Ser Phe
      85                      90                      95

```

```

Ile Pro Ile Leu Gly Leu Val Leu Arg Thr Leu Tyr Met Cys Leu Phe
      100                      105                      110

```

```

Thr Ser Gly Leu Pro Ala Ile Ala Phe Leu Pro Phe Phe Pro Ile Leu
      115                      120                      125

```

```

Arg Ile Lys Lys Lys Asn Tyr Arg Ala Ser Lys Gly Gly Gly Arg Lys

```

130

135

140

Gln Lys Ser Asn Phe Ile Ile Pro Val

145

150

<210> 71

<211> 2020

<212> DNA

<213> Homo sapiens

<400> 71

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```

<210> 72

<211> 104

<212> PRT

<213> Homo sapiens

<400> 72

```

Met Ala Val Gly Pro Ala Gln Ala Ser Thr Gly Ser Leu Leu Ser Leu
  1             5             10             15

```

```

Gln Tyr Ala Pro Ala Leu Pro Pro Pro Ala Gly Asn Val Leu Ala Ser
      20             25             30

```

```

Gln Pro Ser Thr Ile Cys Ser Pro Ile Leu Leu Arg Gly Gln Pro Ser

```

35 40 45
 Leu Gly His Pro Leu Phe Pro Ser Ser Ser Ala Pro Thr Gln Val Thr
 50 55 60
 Asp Pro Ala Asp Ser Phe Ser Leu Gly Lys Val Gly Cys Cys Leu Thr
 65 70 75 80
 Ser Pro Ser Ser Pro Pro Pro Ile His Thr His Arg His Pro Pro Thr
 85 90 95
 Pro Gly Arg Leu Val Ser His Met
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<210> 73
 <211> 760
 <212> DNA
 <213> Homo sapiens

<400> 73
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<210> 74
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 74
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 Gln Lys Leu Ala Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala
 20 25 30
 Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr
 35 40 45
 Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys Leu Leu Thr Leu
 50 55 60
 Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu Pro Val
 65 70 75 80
 Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys Ile Lys
 85 90 95
 Arg His Ala Lys Asn Asn

100

<210> 75
 <211> 875
 <212> DNA
 <213> Homo sapiens

<400> 75
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<210> 76
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 76
 Met Leu Leu Leu Ser Ala Ser Gly Ser Pro Arg Val Leu Gly Asp Val
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 20 25 30
 Ala Glu Gly Ala Gly Leu Arg Leu Cys Thr Cys Ser Leu His Ala Thr
 35 40 45
 Leu Gly Leu Cys Trp Arg Arg Ser Pro Ser Phe Trp Val Gln Thr Ala
 50 55 60
 Pro Pro Asp Ala Val Leu Met Ser Ile Phe Gln Glu Arg Asp Gly Leu
 65 70 75 80
 Gly Ser Arg Glu Trp Arg Gly Leu Pro Leu Pro Cys Arg Ser Trp Pro
 85 90 95
 Met Ala Pro Tyr Pro Ala Ala Leu Gly Phe Trp Pro Glu Ala Asn Ser
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<210> 77
 <211> 2848
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> (2526)

<400> 77

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2848

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<210> 78

<211> 532

<212> PRT

<213> Homo sapiens

<400> 78

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1

5

10

15

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 Lys Ser Phe Glu Val Glu Leu Lys Asp Ala Glu Pro Asp Ile Ile Glu
 35 40 45
 Gln Leu Val Glu Phe Ala Tyr Thr Ala Arg Ile Ser Val Asn Ser Asn
 50 55 60
 Asn Val Gln Ser Leu Leu Asp Ala Ala Asn Gln Tyr Gln Ile Glu Pro
 65 70 75 80
 Val Lys Lys Met Cys Val Asp Phe Leu Lys Glu Gln Val Asp Ala Ser
 85 90 95
 Asn Cys Leu Gly Ile Ser Val Leu Ala Glu Cys Leu Asp Cys Pro Glu
 100 105 110
 Leu Lys Ala Thr Ala Asp Asp Phe Ile His Gln His Phe Thr Glu Val
 115 120 125
 Tyr Lys Thr Asp Glu Phe Leu Gln Leu Asp Val Lys Arg Val Thr His
 130 135 140
 Leu Leu Asn Gln Asp Thr Leu Thr Val Arg Ala Glu Asp Gln Val Tyr
 145 150 155 160
 Asp Ala Ala Val Arg Trp Leu Lys Tyr Asp Glu Pro Asn Arg Gln Pro
 165 170 175
 Phe Met Val Asp Ile Leu Ala Lys Val Arg Phe Pro Leu Ile Ser Lys
 180 185 190
 Asn Phe Leu Ser Lys Thr Val Gln Ala Glu Pro Leu Ile Gln Asp Asn
 195 200 205
 Pro Glu Cys Leu Lys Met Val Ile Ser Gly Met Arg Tyr His Leu Leu
 210 215 220
 Ser Pro Glu Asp Arg Glu Glu Leu Val Asp Gly Pro Arg Pro Arg Arg
 225 230 235 240
 Lys Lys His Asp Tyr Arg Ile Ala Leu Phe Gly Gly Ser Gln Pro Gln
 245 250 255
 Ser Cys Arg Tyr Phe Asn Pro Lys Asp Tyr Ser Trp Thr Asp Ile Arg
 260 265 270
 Cys Pro Phe Glu Lys Pro Arg Asp Ala Ala Cys Val Phe Trp Asp Asn
 275 280 285
 Val Val Tyr Ile Leu Gly Gly Ser Gln Leu Phe Pro Ile Lys Arg Met
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 Asp Cys Tyr Asn Val Val Lys Asp Ser Trp Tyr Ser Lys Leu Gly Pro
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Tyr Thr Ser Gly Gly Ser Glu Val Gly Asn Ser Ala Leu Tyr Leu Phe
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 Glu Cys Tyr Asp Thr Arg Thr Glu Ser Trp His Thr Lys Pro Ser Met
 355 360 365
 Leu Thr Gln Arg Cys Ser His Gly Met Val Glu Ala Asn Gly Leu Ile
 370 375 380
 Tyr Val Cys Gly Gly Ser Leu Gly Asn Asn Val Ser Gly Arg Val Leu
 385 390 395 400
 Asn Ser Cys Glu Val Tyr Asp Pro Ala Thr Glu Thr Trp Thr Glu Leu
 405 410 415
 Cys Pro Met Ile Glu Ala Arg Lys Asn His Gly Leu Val Phe Val Lys
 420 425 430
 Asp Lys Ile Phe Ala Val Gly Gly Gln Asn Gly Leu Gly Gly Leu Asp
 435 440 445
 Asn Val Glu Tyr Tyr Asp Ile Lys Leu Asn Glu Trp Lys Met Val Ser
 450 455 460
 Pro Met Pro Trp Lys Gly Val Thr Val Lys Cys Ala Ala Val Gly Ser
 465 470 475 480
 Ile Val Tyr Val Leu Ala Gly Phe Gln Gly Val Gly Arg Leu Gly His
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 Ile Leu Gln Tyr Asn Thr Glu Thr Asp Lys Trp Val Ala Asn Ser Gln
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 Val Arg Ala Phe Pro Val Thr Lys Leu Phe Asn Leu Cys Cys Arg Tyr
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (2168)

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<210> 80

<211> 525

<212> PRT

<213> Homo sapiens

<400> 80

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Met Ser Arg Tyr Tyr Leu Glu Leu Phe Gln Cys Pro Thr Cys Met Lys
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Gly Ala Trp Ser Leu Val Glu Val Leu Ile Arg Ser Cys Leu Phe Asn
      20              25              30

Glu Ser Phe Cys His Gln Ile Ser Glu Asn Ile Gly Ser Lys Val Leu
      35              40              45

His Leu Thr Leu Leu Lys Phe Phe Phe Asn Leu Ile Glu Ser Glu Val
      50              55              60

Gln His Leu Ser Gln Lys Leu Tyr Asp Trp Ser Asp Ser Gln Asn Leu
      65              70              75              80

Lys Ile Thr Gly Lys Ala Met Leu Leu Glu Ile Phe Trp Ser Gly Ser
      85              90              95

Glu Thr Ser Gly Leu Leu Thr Lys Pro Val Asn Met Leu Leu Glu Trp
      100             105             110

Thr Ile Tyr Ser His Lys Glu Lys Phe Lys Ser Asn Asp Thr Phe Leu
      115             120             125

```

Pro Gln Glu Leu Glu Ile Phe Ile Cys Ser Phe Ser Ser Ser Trp Leu
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 165 170 175
 Ser Tyr Leu Pro Ala Leu Gly Lys Thr Gly Val Leu Gly Ser Gly Lys
 180 185 190
 Ile Gln Val Ser Lys Lys Ile Gly Gln Arg Pro Cys Phe Asp Ser Gln
 195 200 205
 Arg Thr Leu Leu Met Leu Asn Gly Thr Lys Gln Lys Gln Val Glu Gly
 210 215 220
 Leu Pro Glu Leu Leu Asp Leu Asn Leu Ala Lys Cys Ser Ser Ser Leu
 225 230 235 240
 Lys Lys Leu Lys Lys Lys Ser Glu Gly Glu Leu Ser Cys Ser Lys Glu
 245 250 255
 Asn Cys Pro Ser Val Val Lys Lys Met Asn Phe His Lys Thr Asn Leu
 260 265 270
 Lys Gly Glu Thr Ala Leu His Arg Ala Cys Ile Asn Asn Gln Val Glu
 275 280 285
 Lys Leu Ile Leu Leu Leu Ser Leu Pro Gly Ile Asp Ile Asn Val Lys
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 Asp Asn Ala Gly Trp Thr Pro Leu His Glu Ala Cys Asn Tyr Gly Asn
 305 310 315 320
 Thr Val Gly Val Gln Glu Ile Leu Gln Arg Cys Pro Glu Val Asp Leu
 325 330 335
 Leu Thr Gln Val Asp Gly Val Thr Pro Leu His Asp Ala Leu Ser Asn
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 Gly His Val Glu Ile Gly Lys Leu Leu Leu Gln His Gly Gly Pro Val
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 Val Ser Pro Gln Ile Lys Glu Glu Leu Phe Ala Ile Thr Lys Ile Glu
 385 390 395 400
 Asp Thr Val Glu Asn Phe His Ala Gln Ala Glu Lys His Phe His Tyr
 405 410 415
 Gln Gln Leu Glu Phe Gly Ser Phe Leu Leu Ser Arg Met Leu Leu Asn
 420 425 430
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 435 440 445

Gly Leu Thr His Leu Asn Glu Leu Leu Met Ala Cys Lys Ser His Lys
450 455 460

Glu Thr Thr Ser Val His Thr Asp Trp Leu Leu Asp Leu Tyr Ala Gly
465 470 475 480

Asn Ile Lys Thr Leu Gln Lys Leu Pro His Ile Leu Lys Glu Leu Pro
485 490 495

Glu Asn Leu Lys Val Cys Pro Gly Val His Thr Glu Ala Leu Met Ile
500 505 510

Thr Leu Glu Met Met Cys Arg Ser Val Met Glu Phe Ser
515 520 525

<210> 81

<211> 2625

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (2559)

<220>

<221> unsure

<222> (2561)

<400> 81

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```

<210> 82

<211> 490

<212> PRT

<213> Homo sapiens

<400> 82

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Met Leu Trp Arg Ala Leu Ala Val Glu Pro Arg Leu Ala Ala Gln Val
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```

```

Leu Gly Leu Leu Leu Glu Lys Met Ser Arg Asp Val Pro Phe Lys Glu
          20              25              30

```

```

Ser Arg Ala Phe Leu Leu Gly Arg Thr Pro Asp Arg Val Ala Thr Leu
      35              40              45

```

```

Leu Pro Leu Ser Ala Thr Cys Ala Leu Phe Glu Val Met Ser Thr Pro
      50              55              60

```

```

Ala Ala Gly Pro Ala Val Leu Glu Leu Tyr Pro Gln Leu Phe Val Val
      65              70              75              80

```

```

Leu Leu Leu Arg Val Ser Cys Thr Val Gly Val Gln Leu Pro Arg Asn
          85              90              95

```

```

Leu Gln Ala Gln Glu Arg Arg Gly Ala Ser Pro Ala Leu Ala Thr Arg
      100             105             110

```

```

Asn Leu Glu Pro Cys Ser Ser Ala Val Asp Thr Leu Arg Ser Met Leu
      115             120             125

```

```

Leu Arg Ser Gly Ser Glu Asp Val Val Gln Arg Met Asp Leu Glu Gly
      130             135             140

```

```

Gly Trp Glu Leu Leu Arg Thr Ser Ala Gly His Glu Glu Gly Ala Thr
      145             150             155             160

```

```

Arg Leu Ala Arg Ala Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu
      165             170             175

```

```

Val Leu Lys Thr Leu Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln
      180             185             190

```

```

Arg Val Thr Thr Thr Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val
      195             200             205

```

WO 00/09552

PCT/US99/18298

Ala Asn Asp Leu Met Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala
210 215 220

Arg Gln Lys Asp Thr Cys Ala Ser Val Arg Arg Leu Val Leu Arg Gly
225 230 235 240

Leu Ala Asn Leu Ala Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly
245 250 255

Pro Gln Leu Leu Thr Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn
260 265 270

Pro His Ser Pro Val Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu
275 280 285

Val His Leu Val Glu Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val
290 295 300

Ala Ile Arg Ile Arg Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg
305 310 315 320

Thr Ala Ser Ile Arg Leu Phe Gly His Leu Asn Lys Val Cys His Gly
325 330 335

Asp Cys Glu Asp Val Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro
340 345 350

Leu Leu Leu His Leu Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys
355 360 365

Arg Phe Ala Leu Arg Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu
370 375 380

Ser Ala Ala Phe Gln Lys His Leu Gln Glu Gly Arg Ala Leu His Phe
385 390 395 400

Gly Glu Phe Leu Asn Thr Thr Cys Lys His Leu Met His His Phe Pro
405 410 415

Asp Leu Leu Gly Arg Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser
420 425 430

Ser Trp Glu Asn Val Arg Ala Ala Ala Pro Leu Phe Thr Gly Lys His
435 440 445

His Pro Leu Pro His Pro His Ala Ala Arg Gln Pro Arg Leu Met Pro
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Pro Leu His Arg Val Pro Gly Ala Ala Leu Gly Ala Gln Ala Ala Ala
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Ala Gly Gly Pro Gly Pro Ala His Cys Gly
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<210> 83

<211> 1476

<212> DNA

<213> Homo sapiens

<400> 83

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<210> 84

<211> 382

<212> PRT

<213> Homo sapiens

<400> 84

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Met Ser Glu Pro Pro Ile Ala His Leu Leu Arg Pro Val Leu Pro Arg
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Ala Phe Ala Phe Pro Val Asp Pro Gln Val Gln Ser Ala Ala Asp Glu
          20             25             30

Thr Ala Val Gln Leu Ser Glu Leu Leu Thr Leu Pro Val Leu Met Lys
 35             40             45

Arg Ser Ile Thr Ala Pro Leu Ala Ala His Ile Ser Leu Val Asn Lys
 50             55             60

Ala Ala Val Asp Tyr Phe Phe Val Glu Leu His Leu Glu Ala His Tyr
 65             70             75             80

Glu Ala Leu Arg His Phe Leu Leu Met Glu Asp Gly Glu Phe Ala Gln
          85             90             95

Ser Leu Ser Asp Leu Leu Phe Glu Lys Leu Gly Ala Gly Gln Thr Pro
100             105             110

Arg Arg Ala Ala Gln Pro Ala Gly Ala Glu Leu Cys Ala Asp Lys Ala
115             120             125

Leu Gln Cys Ser Leu His Gly Asp Thr Pro His Ala Ser Asn Leu Ser
130             135             140

```

WO 00/09552

PCT/US99/18298

Leu Ala Leu Lys Tyr Leu Pro Glu Val Phe Ala Pro Asn Ala Pro Asp
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Val Leu Ser Cys Leu Glu Leu Arg Tyr Lys Val Asp Trp Pro Leu Asn
 165 170 175

Ile Val Ile Thr Glu Gly Cys Leu Ser Lys Tyr Ser Gly Val Phe Ser
 180 185 190

Phe Leu Leu Gln Leu Lys Leu Met Met Trp Ala Leu Lys Asp Val Cys
 195 200 205

Phe His Leu Lys Arg Thr Ala Leu Leu Ser His Met Ala Gly Ser Val
 210 215 220

Gln Phe Arg Gln Leu Gln Leu Phe Lys His Glu Met Gln His Phe Val
 225 230 235 240

Lys Val Ile Gln Gly Tyr Ile Ala Asn Gln Ile Leu His Val Thr Trp
 245 250 255

Cys Glu Phe Arg Ala Arg Leu Ala Thr Val Gly Asp Leu Glu Glu Ile
 260 265 270

Gln Arg Ala His Ala Glu Tyr Leu His Lys Ala Val Phe Arg Gly Leu
 275 280 285

Leu Thr Glu Lys Ala Ala Pro Val Met Asn Val Ile His Ser Ile Phe
 290 295 300

Ser Leu Val Leu Lys Phe Arg Ser Gln Leu Ile Ser Gln Ala Trp Gly
 305 310 315 320

Pro Pro Gly Gly Pro Arg Gly Ala Glu His Pro Asn Phe Ala Leu Met
 325 330 335

Gln Gln Ser Tyr Asn Thr Phe Lys Tyr Tyr Ser His Phe Leu Phe Lys
 340 345 350

Val Val Thr Lys Leu Val Asn Arg Gly Tyr Gln Pro His Leu Glu Asp
 355 360 365

Phe Leu Leu Arg Ile Asn Phe Asn Asn Tyr Tyr Gln Asp Ala
 370 375 380

<210> 85
 <211> 1212
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (1146)..(1147)

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1212

<210> 86

<211> 167

<212> PRT

<213> Homo sapiens

<400> 86

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Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val Ala Leu
  1             5             10             15

```

```

Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro Arg Leu
          20             25             30

```

```

Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Tyr Lys Ser Tyr Val
      35             40             45

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```

Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu Leu
      50             55             60

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```

Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr
      65             70             75             80

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```

Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu
          85             90             95

```

```

Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu
      100             105             110

```

```

Lys Arg Tyr Ala His Ala Leu Val Phe Gly Ile Leu Leu Thr Cys Arg
      115             120             125

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Leu Leu Ile Ala Arg Lys Pro Glu Asp Arg Ser Ser Glu Lys Lys Pro
      130             135             140

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Leu Pro Gly Asn Ala Glu Glu Gln Pro Ser Leu Tyr Glu Lys Ala Pro
      145             150             155             160

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Gln Gly Lys Val Lys Val Ser
          165

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<210> 87

<211> 1059

<212> DNA

<213> Homo sapiens

<400> 87

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<210> 88

<211> 192

<212> PRT

<213> Homo sapiens

<400> 88

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Met Thr Lys Gly Ile Thr Phe Leu Asn Leu Asp Tyr Tyr Val Ala Val
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Tyr Leu Pro Gly His Phe Phe His Leu Leu Asn Val Gln His Pro Asp
          20             25             30

Leu Ile Cys His Asn Leu Phe Leu Thr Gly Asn Asn Glu Met Ile Asp
          35             40             45

Met Leu Pro His Cys Pro Leu Gln Ser Leu Ser Gly Ser Leu Val Leu
          50             55             60

Asp Cys Cys Ser Gly Lys Leu Tyr Arg Ala Leu Leu Ser Gln Ser Ser
          65             70             75             80

Leu Leu Gln Leu Leu Gln Asn Thr Cys Leu Asp Cys Glu Lys Met Ala
          85             90             95

Ala Leu His Cys Ala Leu Tyr Cys Gly Gln Gly Ala Gln Phe Leu Glu
          100            105            110

Ala Gln Ile Ile Gln Trp Ile Ser Glu Asn Val Ser Ala Cys His Ser
          115            120            125

Phe Asp Leu Ile Gln Glu Phe Ile Ile Ala Ser Ser Tyr Trp Ser Val
          130            135            140

Tyr Ser Glu Thr Ser Asn Met Asp Lys Leu Leu Pro His Ser Ser Val
          145            150            155            160

Leu Thr Trp Asn Thr Glu Ile Pro Gly Ile Thr Leu Val Thr Glu Asp

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165

170

175

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<210> 89

<211> 2529

<212> DNA

<213> Homo sapiens

<400> 89

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<210> 90

<211> 244

<212> PRT

<213> Homo sapiens

<400> 90

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 20 25 30
 Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe Thr Val Ile Tyr Asn
 35 40 45
 Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe Ser Asn Leu Gln Glu
 50 55 60
 Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu Glu Val Gly Cys Gly
 65 70 75 80
 Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys
 85 90 95
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 Glu Asn Arg His Leu Gln Phe Glu Arg Phe Val Val Ala Ala Gly Glu
 115 120 125
 Asn Met His Gln Val Ala Asp Gly Ser Val Asp Val Val Val Cys Thr
 130 135 140
 Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg Ile Leu Arg Glu Val
 145 150 155 160
 Cys Arg Val Leu Arg Pro Gly Gly Ala Phe Tyr Phe Met Glu His Val
 165 170 175
 Ala Ala Glu Cys Ser Thr Trp Asn Tyr Phe Trp Gln Gln Val Leu Asp
 180 185 190
 Pro Ala Trp His Leu Leu Phe Asp Gly Cys Asn Leu Thr Arg Glu Ser
 195 200 205
 Trp Lys Ala Leu Glu Arg Ala Ser Phe Ser Lys Leu Lys Leu Gln His
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 Ile Gln Ala Pro Leu Ser Trp Glu Leu Val Arg Pro His Ile Tyr Gly
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<210> 91

<211> 2390

<212> DNA

<213> Homo sapiens

<400> 91

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<210> 92

<211> 212

<212> PRT

<213> Homo sapiens

<400> 92

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Met Thr Gly Ala Phe Tyr Ser Val Ser Thr Leu Leu Asn Gln Met Ile
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Leu Thr Tyr Tyr Glu Gly Glu Glu Val Asn Ala Gly Arg Ile Gly Leu
  20              25              30

Thr Leu Val Val Ala Gly Met Val Gly Ser Ile Leu Cys Gly Leu Trp
  35              40              45

Leu Asp Tyr Thr Lys Thr Tyr Lys Gln Thr Thr Leu Ile Val Tyr Ile
  50              55              60

Leu Ser Phe Ile Gly Met Val Ile Phe Thr Phe Thr Leu Asp Leu Arg
  65              70              75              80

Tyr Ile Ile Ile Val Phe Val Thr Gly Gly Val Leu Gly Phe Phe Met

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<210> 93
<211> 2922
<212> DNA
<213> Homo sapiens
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[illegible]

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<210> 94

<211> 451

<212> PRT

<213> Homo sapiens

<400> 94

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Met Ala Thr Tyr Thr Cys Ile Thr Cys Arg Val Ala Phe Arg Asp Ala
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Asp Met Gln Arg Ala His Tyr Lys Thr Asp Trp His Arg Tyr Asn Leu
          20             25             30

Arg Arg Lys Val Ala Ser Met Ala Pro Val Thr Ala Glu Gly Phe Gln
          35             40             45

Glu Arg Val Arg Ala Gln Arg Ala Val Ala Glu Glu Glu Ser Lys Gly
          50             55             60

Ser Ala Thr Tyr Cys Thr Val Cys Ser Lys Lys Phe Ala Ser Phe Asn
          65             70             75             80

Ala Tyr Glu Asn His Leu Lys Ser Arg Arg His Val Glu Leu Glu Lys
          85             90             95

Lys Ala Val Gln Ala Val Asn Arg Lys Val Glu Met Met Asn Glu Lys
          100            105            110

Asn Leu Glu Lys Gly Leu Gly Val Asp Ser Val Asp Lys Asp Ala Met
          115            120            125

Asn Ala Ala Ile Gln Gln Ala Ile Lys Ala Gln Pro Ser Met Ser Pro
          130            135            140

Lys Lys Ala Pro Pro Ala Pro Ala Lys Glu Ala Arg Asn Val Val Ala
          145            150            155            160

Val Gly Thr Gly Gly Arg Gly Thr His Asp Arg Asp Pro Ser Glu Lys

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PCT/US99/18298

<210>	95
<211>	1395
<212>	DNA

<213> Homo sapiens

<400> 95

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<210> 96

<211> 137

<212> PRT

<213> Homo sapiens

<400> 96

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Met Arg Val Ile Ser Gln Arg Tyr Pro Asp Ile Arg Ile Glu Gly Glu
  1             5             10             15

Asn Tyr Leu Pro Gln Pro Ile Tyr Arg His Ile Ala Ser Phe Leu Ser
      20             25             30

Val Phe Lys Leu Val Leu Ile Gly Leu Ile Ile Val Gly Lys Asp Pro
      35             40             45

Phe Ala Phe Phe Gly Met Gln Ala Pro Ser Ile Trp Gln Trp Gly Gln
      50             55             60

Glu Asn Lys Val Tyr Ala Cys Met Met Val Phe Phe Leu Ser Asn Met
      65             70             75             80

Ile Glu Asn Gln Cys Met Ser Thr Gly Ala Phe Glu Ile Thr Leu Asn
      85             90             95

Asp Val Pro Val Trp Ser Lys Leu Glu Ser Gly His Leu Pro Ser Met
      100            105            110

Gln Gln Leu Val Gln Ile Leu Asp Asn Glu Met Lys Leu Asn Val His
      115            120            125

Met Asp Ser Ile Pro His His Arg Ser
      130            135

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<210> 97
 <211> 1299
 <212> DNA
 <213> Homo sapiens

<400> 97
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 ggcttttttca tctttaagag acctgagtc tcaagaaaat ccttttcttg aagtatctgc 180
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<210> 98
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 98
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 35 40 45
 Tyr Ile Asn Glu Ser Thr Glu Ala Gln Ser Glu Gln Lys Glu Lys Ser
 50 55 60
 Leu Glu Phe Thr Lys Glu Leu Pro Gly Tyr Gly Tyr Thr Lys Lys Leu
 65 70 75 80
 Ile Leu Ala Leu Ile Val Thr Gly Ile Leu Thr Ile Leu Ile Ile Leu
 85 90 95
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 Glu Glu Gly Phe Ser Arg Asp Ser Glu Ala Pro Thr Glu Glu Glu Ser
 115 120 125

Glu Ala Leu Pro
130

<210> 99
<211> 915
<212> DNA
<213> Homo sapiens

<400> 99
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<210> 100
<211> 76
<212> PRT
<213> Homo sapiens

<400> 100
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Ala Cys His Ser Arg Ser Ala Asp Val Asp Ser Leu Ser Glu Ser Ser
35 40 45
Pro Asn Ser Ser Pro Gly Pro Cys Pro Glu Lys Ala Pro Pro Pro Gln
50 55 60
Lys Pro Ser His Glu Gly Ser Tyr Leu Leu Gln Pro
65 70 75

<210> 101
<211> 2915
<212> DNA
<213> Homo sapiens

<400> 101
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gcttcaccct ccgagtagct gggattacag gtgtgcacca ccacaccgg ctaatttttg 240

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<210> 102

<211> 104

<212> PRT

<213> Homo sapiens

<400> 102

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Met Phe Ile Gln Asn Leu Leu Trp Glu Lys Asn Val Arg Asn Lys Asp
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Asn His Cys Met Glu Val Ile Arg Leu Lys Gly Leu Val Ser Ile Lys
      20             25             30

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Asp Lys Ser Gln Gln Val Ile Val Gln Gly Val His Glu Leu Tyr Asp
      35             40             45

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Leu Glu Glu Thr Pro Val Ser Trp Lys Asp Asp Thr Glu Arg Thr Asn
50 55 60

Arg Leu Val Leu Ile Gly Arg Asn Leu Asp Lys Asp Ile Leu Lys Gln
65 70 75 80

Leu Phe Ile Ala Thr Val Thr Glu Thr Glu Lys Gln Trp Thr Thr His
85 90 95

Phe Lys Glu Asp Gln Val Cys Thr
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<210> 103

<211> 1530

<212> DNA

<213> Homo sapiens

<400> 103

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<210> 104

<211> 215

<212> PRT

<213> Homo sapiens

<400> 104

Met Leu Tyr Thr Thr Ser Leu Met Arg Thr Val Tyr Lys Pro Ser Leu
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Met Arg Thr Leu Tyr Met Ala Ser Leu Thr Arg Thr Leu Tyr Lys Ala
20 25 30

Leu Leu Thr Arg Thr Leu Tyr Thr Thr Ser Leu Met Arg Thr Pro Tyr

35 40 45
 Lys Thr Ser Pro Met Arg Met Leu Tyr Met Thr Ser Leu Met Ala Pro
 50 55 60
 Thr Arg His Ala Asn Glu Asp Ala Val Asp Asp Ile Ala Tyr Lys Asp
 65 70 75 80
 Thr Val Gln Asp Ile Ala Asn Glu Asp Ala Val Tyr Asp Ile Ala Asn
 85 90 95
 Glu Asp Val Val Tyr Asp Ile Ala Asn Glu Asp Ala Leu Gln Asp Ile
 100 105 110
 Ala Asn Glu Val Ala Val Tyr Asp Ile Ala Asn Glu Asp Ile Val Tyr
 115 120 125
 Asp Ile Ala Asn Glu Asp Ala Leu Tyr Asp Ile Thr Asn Glu Asp Ala
 130 135 140
 Val Tyr Asn Ile Ala Asn Glu Asp Ala Val Tyr Gly Ile Ala Asn Glu
 145 150 155 160
 Asp Ala Val Tyr Glu Phe Ala Asn Lys Asp Ala Val Tyr Asp Ile Ala
 165 170 175
 Asn Glu Asp Thr Val Gln Asp Ile Cys Lys Lys Glu Asp Ala Ala Asn
 180 185 190
 Glu Pro Leu Thr Leu Glu Asn Asp Thr Tyr Pro Glu Ile Thr His Phe
 195 200 205
 Leu Arg Lys Lys Arg His Leu
 210 215

<210> 105
 <211> 2423
 <212> DNA
 <213> Homo sapiens

<400> 105
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<210> 106

<211> 66

<212> PRT

<213> Homo sapiens

<400> 106

Met Val Lys Leu Ser Ile Val Leu Thr Pro Gln Phe Leu Ser His Asp

1

5

10

15

Gln Gly Gln Leu Thr Lys Glu Leu Gln Gln His Val Lys Ser Val Thr

20

25

30

Cys Pro Cys Glu Tyr Leu Arg Lys Val Ser Glu Cys Arg Gln Met Gly

35

40

45

Pro Gly Ala Leu Glu Gln Phe Pro Gly Leu Ser Cys His Thr Ser His

50

55

60

Ser Arg

65

<210> 107

<211> 1418

<212> DNA

<213> Homo sapiens

<400> 107

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<210> 108

<211> 123

<212> PRT

<213> Homo sapiens

<400> 108

Met Asn Arg Gly Leu Pro Val Leu Lys Ala Gln Val Phe Ile Leu Tyr
 1 5 10 15

Leu Ser Arg Ala His Thr Lys Ile Gln Pro Ser Asn Lys His Asp Gly
 20 25 30

Ala Val Pro Leu Pro Ala Ser Pro Val Pro Leu Ser Pro Pro Gly Leu
 35 40 45

Gly Ser Ser Gly Val Gly Val Gly Arg Gly Pro Cys Pro Pro Cys Leu
 50 55 60

Asp Phe Ala Pro Leu Gly Pro Ala Gly Ser Arg Pro Val Asn Val Ser
 65 70 75 80

Ser Ser Gly Thr Asp Ser Val Cys Ser Trp Pro Trp Val His Leu Thr
 85 90 95

Asn Ile Cys Pro Gly Pro Pro Arg Pro Ser Pro Met Pro Pro Gly Pro
 100 105 110

Arg His Leu Phe Glu Val Leu Pro Met Cys Ser
 115 120

<210> 109

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 109

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<210> 110

<211> 283

<212> PRT

<213> Homo sapiens

<400> 110

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 20 25 30

Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn
 35 40 45

Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Glu Leu
 50 55 60

Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr
 65 70 75 80

Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu
 85 90 95

Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp
 100 105 110

Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile
 115 120 125

Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu
 130 135 140

Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser
 145 150 155 160

Ser Ala Leu Ala Trp Leu Thr Leu Glu Val Leu Ala Ile Leu Leu Ser
 165 170 175

Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val
 180 185 190

Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met
 195 200 205

Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Trp Cys
 210 215 220

Cys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile
 225 230 235 240

Leu Ala Asp Ala Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn
 245 250 255

Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met
 260 265 270

Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg
 275 280

<210> 111
 <211> 2024
 <212> DNA
 <213> Homo sapiens

<400> 111
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<210> 112
 <211> 487
 <212> PRT

<213> Homo sapiens

<400> 112

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 Arg Ala Val Met Gln Ser Gln Lys Pro Pro Lys Asn Cys Arg Glu Ala
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 35 40 45
 Glu Asn Thr Arg Pro Lys Phe Leu Ser Arg Asp Val Asp Ser Glu Ile
 50 55 60
 Ser Asp Leu Glu Asn Glu Val Glu Asn Lys Thr Ala Gln Ile Leu Asn
 65 70 75 80
 Leu Gln Gln His Leu Ser Ala Leu Glu Lys Asp Ile Lys His Asn Glu
 85 90 95
 Glu Leu Leu Lys Arg Cys Gln Leu His Tyr Lys Glu Leu Lys Met Lys
 100 105 110
 Ile Arg Lys Asn Ile Ser Glu Ile Arg Glu Leu Glu Asn Ile Glu Glu
 115 120 125
 His Gln Ser Val Asp Ile Ala Thr Leu Glu Asp Glu Ala Gln Glu Asn
 130 135 140
 Lys Ser Lys Met Lys Met Val Glu Glu His Met Glu Gln Gln Lys Glu
 145 150 155 160
 Asn Met Glu His Leu Lys Ser Leu Lys Ile Glu Ala Glu Asn Lys Tyr
 165 170 175
 Asp Ala Ile Lys Phe Lys Ile Asn Gln Leu Ser Glu Leu Ala Asp Pro
 180 185 190
 Leu Lys Asp Glu Leu Asn Leu Ala Asp Ser Glu Val Asp Asn Gln Lys
 195 200 205
 Arg Gly Lys Arg His Tyr Glu Glu Lys Gln Lys Glu His Leu Asp Thr
 210 215 220
 Leu Asn Lys Lys Lys Arg Glu Leu Asp Met Lys Glu Lys Glu Leu Glu
 225 230 235 240
 Glu Lys Met Ser Gln Ala Arg Gln Ile Cys Pro Glu Arg Ile Glu Val
 245 250 255
 Glu Lys Ser Ala Ser Ile Leu Asp Lys Glu Ile Asn Arg Leu Arg Gln
 260 265 270
 Lys Ile Gln Ala Glu His Ala Ser His Gly Asp Arg Glu Glu Ile Met
 275 280 285
 Arg Gln Tyr Gln Glu Ala Arg Glu Thr Tyr Leu Asp Leu Asp Ser Lys
 290 295 300

Val Arg Thr Leu Lys Lys Phe Ile Lys Leu Leu Gly Glu Ile Met Glu
 305 310 315 320
 His Arg Phe Lys Thr Tyr Gln Gln Phe Arg Arg Cys Leu Thr Leu Arg
 325 330 335
 Cys Lys Leu Tyr Phe Asp Asn Leu Leu Ser Gln Arg Ala Tyr Cys Gly
 340 345 350
 Lys Met Asn Phe Asp His Lys Asn Glu Thr Leu Ser Ile Ser Val Gln
 355 360 365
 Pro Gly Glu Gly Asn Lys Ala Ala Phe Asn Asp Met Arg Ala Leu Ser
 370 375 380
 Gly Gly Glu Arg Ser Phe Ser Thr Val Cys Phe Ile Leu Ser Leu Trp
 385 390 395 400
 Ser Ile Ala Glu Ser Pro Phe Arg Cys Leu Asp Glu Phe Asp Val Tyr
 405 410 415
 Met Asp Met Val Asn Arg Arg Ile Ala Met Asp Leu Ile Leu Lys Met
 420 425 430
 Ala Asp Ser Gln Arg Phe Arg Gln Phe Ile Leu Leu Thr Pro Gln Ser
 435 440 445
 Met Ser Ser Leu Pro Ser Ser Lys Leu Ile Arg Ile Leu Arg Met Ser
 450 455 460
 Asp Pro Glu Arg Gly Gln Thr Thr Leu Pro Phe Arg Pro Val Thr Gln
 465 470 475 480
 Glu Glu Asp Asp Asp Gln Arg
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<210> 113
 <211> 1424
 <212> DNA
 <213> Homo sapiens

<400> 113
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<210> 114

<211> 207

<212> PRT

<213> Homo sapiens

<400> 114

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Met Gly Lys Cys Ser Gly Arg Cys Thr Leu Val Ala Phe Cys Cys Leu
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Gln Leu Val Ala Ala Leu Glu Arg Gln Ile Phe Asp Phe Leu Gly Tyr
      20             25             30

Gln Trp Ala Pro Ile Leu Ala Asn Phe Leu His Ile Met Ala Val Ile
      35             40             45

Leu Gly Ile Phe Gly Thr Val Gln Tyr Arg Ser Arg Tyr Leu Ile Leu
      50             55             60

Tyr Ala Ala Trp Leu Val Leu Trp Val Gly Trp Asn Ala Phe Ile Ile
      65             70             75             80

Cys Phe Tyr Leu Glu Val Gly Gln Leu Ser Gln Asp Arg Asp Phe Ile
      85             90             95

Met Thr Phe Asn Thr Ser Leu His Arg Ser Trp Trp Met Glu Asn Gly
      100            105            110

Pro Gly Cys Leu Val Thr Pro Val Leu Asn Ser Arg Leu Ala Leu Glu
      115            120            125

Asp His His Val Ile Ser Val Thr Gly Cys Leu Leu Asp Tyr Pro Tyr
      130            135            140

Ile Glu Ala Leu Ser Ser Ala Leu Gln Ile Phe Leu Ala Leu Phe Gly
      145            150            155            160

Phe Val Phe Ala Cys Tyr Val Ser Lys Val Phe Leu Glu Glu Glu Asp
      165            170            175

Ser Phe Asp Phe Ile Gly Gly Phe Asp Ser Tyr Gly Tyr Gln Ala Pro
      180            185            190

Gln Lys Thr Ser His Leu Gln Leu Gln Pro Leu Tyr Thr Ser Gly
      195            200            205

```

<210> 115

<211> 843

<212> DNA

<213> Homo sapiens

<400> 115

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tagtgactgt cattgccatt caagaatgtt tgattagttt atattccctt cgtagtgac 720
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843

<210> 116

<211> 84

<212> PRT

<213> Homo sapiens

<400> 116

```

Met Gly Thr Arg Arg Pro Leu Gly Arg Leu Leu Gln Ala Gly Thr Arg
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```

```

Pro Ala Arg Pro Thr Pro His Gly Arg Arg Arg Leu His Val Ser Ala
          20             25             30

```

```

Pro Leu Gln Ala Gln Glu Ala Arg Gly Val Thr Trp Arg Pro Gly Pro
          35             40             45

```

```

Ala Ser Pro Ala Pro Leu Arg Leu Thr Thr Tyr Pro Pro Pro Phe Phe
          50             55             60

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```

Leu Ser Lys Tyr Pro Asp Gln Ser Ile Ser Pro Arg Arg Thr Arg Thr
          65             70             75             80

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Ala Gly Ser Asp

<210> 117

<211> 2232

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (225)

<400> 117

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tgaccttggg caagtgactc cccatctctg gccctcagga ggttgggcag gtccgggcca 180
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aggagaaggc tgcgcggcag cgggagaagc tccggcgccg agagcaggag gccaagaaga 600
gctaggggag ggtgcacagg cgctggcacc cggcaggggc agccactggc tccgcgggca 660
caggcctcac cagggaggct ggacctgggc gctgcacttg ggctagcctg gtcccacgct 720
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aaaaaaaaaa aa 2232

```

<210> 118

<211> 133

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (8)

<400> 118

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Met Val Gly Glu Glu Glu Xaa Pro Asn Thr Pro Asn Pro His Leu
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Ser Gln Pro His Ser Phe Gln Ile Leu Ala Leu Gly Val Leu Ile His
      20             25            30

Gly Gln Val Thr Val Trp Glu Ala Glu Ala Pro Leu Gln Gly Gly Phe
      35             40            45

Gly Ala Pro Gln Ser Thr Pro Gly Ala Lys Gly Ala Trp Ala Trp Glu
      50             55            60

Ala Arg Thr Gly Lys Val Leu Gly Leu Ser Pro Ser Pro Arg Thr Pro
      65             70            75            80

Pro Gln Ser Leu Gly Leu Ser Asn Ser His Asp Arg Ala Leu Val Lys
      85             90            95

Arg Lys Leu Lys Glu Met Ala Ala Ala Ala Glu Lys Glu Arg Lys Ala
      100            105           110

```

Gln Glu Lys Ala Ala Arg Gln Arg Glu Lys Leu Arg Arg Arg Glu Gln
 115 120 125

Glu Ala Lys Lys Ser
 130

<210> 119

<211> 4086

<212> DNA

<213> Homo sapiens

<400> 119

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aaaaaa
4086

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<210> 120

<211> 102

<212> PRT

<213> Homo sapiens

<400> 120

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Met Ser Thr Gly Asn Thr Val Cys Ser Arg Tyr His Phe Tyr Val Arg
  1                      5                      10                      15

```

```

Val Asn Gln Ala Val Ile Trp Val Asp Val Leu Ile Tyr Trp Ser Val
          20                      25                      30

```

```

His Ile Leu Asp Ile Val Ile Pro His Trp Leu Val Asn Ser Val Ser
    35                      40                      45

```

```

Ile Tyr Trp Ile Ile Glu Trp Arg Leu Trp Cys Trp Trp Trp Glu Arg
    50                      55                      60

```

```

Trp Trp Tyr Trp Arg Ile His Pro Ala Val Val Ala Ala Val Phe Arg
    65                      70                      75                      80

```

```

Ile Lys Asp Asp Arg Ser Ser Ala Pro Cys Asp Ile Gly Ile Met Cys
          85                      90                      95

```

```

Ala Gln Pro Ala Asn Pro
          100

```

<210> 121

<211> 1293

<212> DNA

<213> Homo sapiens

<400> 121

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ggtccagaag aaatgtggct tcagctctgc tgctactgtg cctcccttct cctgcccac 60
tcagcccaca aaataggctg gacactcaaa aaacgttgcg tttatctacc ttttagagag 120

```



```

ggtagaatagc agagaactgg aggtgggaat ggtaaggaac tcccagcagg gtagtggagg 180
gaatgggctg acgcatctaa ggctgatgcc aggtctgtct cctatctggg tggcctcagc 240
aaatgacgtc cagcacatcc aggggcaggc tcaagggaga acagccccc aagctaagat 300
cctgccaaagc taataacagt agttctaatag aaatgtgaga ggctataatc ccatattggga 360
aattcctaaa aagtcattgag gcaggggatt ggtttatgtt attatcatga cctgagagtc 420
atggctcaga gccaaatgtt caggattgaa ttcaacagca tttaaattgtc tttagagcag 480
gatggaaata tgttagcaat gcctgcagag tgccaagtaa acgcaaaagc caatgagatc 540
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```

<210> 122

<211> 54

<212> PRT

<213> Homo sapiens

<400> 122

```

Met Val Arg Asn Ser Gln Gln Gly Ser Gly Gly Asn Gly Leu Thr His
  1                      5                      10                     15

```

```

Leu Arg Leu Met Pro Gly Leu Leu Pro Ile Trp Val Ala Ser Ala Asn
      20                      25                     30

```

```

Asp Val Gln His Ile Gln Gly Gln Ala Gln Gly Arg Thr Ala Pro Lys
    35                      40                     45

```

```

Ala Lys Ile Leu Pro Ser
    50

```

<210> 123

<211> 2509

<212> DNA

<213> Homo sapiens

<400> 123

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cggacgggtg tcagctggtt tccattgtgg ggatggcact atacacagga tacgtcttca 180
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cagtattttc ttaacctttg tgactgtttc aatattacc ccggtgaaagc ttttcttaat 540
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tattgagAAC tacttaacaa aagattttat tgtaagcttg aactcaggag tacagtttta 780
gctatctaga ctctaacagc ttttgcttta aaattattaa agtgtttctt aatgaaaaag 840

```

```

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```

<210> 124

<211> 89

<212> PRT

<213> Homo sapiens

<400> 124

```

Met Ala Gly Met Ala Leu Ala Arg Ala Trp Lys Gln Met Ser Trp Phe
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Tyr Tyr Gln Tyr Leu Leu Val Thr Ala Leu Tyr Met Leu Glu Pro Trp
      20              25              30

Glu Arg Thr Val Phe Ser Trp Phe Pro Leu Trp Gly Trp His Tyr Thr
      35              40              45

Gln Asp Thr Ser Ser Cys Pro Ser Thr Ser Trp Arg Tyr Cys Thr Thr
      50              55              60

Leu Lys Ser Tyr Asn Asp Gln Asp Ala Thr Arg Ile Arg Gly Ser Leu
      65              70              75              80

Gly Lys Thr His Pro Thr Lys Leu Glu
      85

```

<210> 125

<211> 2672

<212> DNA

<213> Homo sapiens

<400> 125

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<210> 126

<211> 750

<212> PRT

<213> Homo sapiens

<400> 126

```

Met Glu Asp Leu Phe Glu Thr Phe Gln Asp Glu Met Gly Phe Ser Asn
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```

Met Glu Asp Asp Gly Pro Glu Glu Glu Arg Val Ala Glu Pro Gln
      20             25             30

```

```

Ala Asn Phe Asn Thr Pro Gln Ala Leu Arg Phe Glu Glu Leu Leu Ala
      35             40             45

```

Asn Leu Leu Asn Glu Gln His Gln Ile Ala Lys Glu Leu Phe Glu Gln
 50 55 60
 Leu Lys Met Lys Lys Pro Ser Ala Lys Gln Gln Lys Glu Val Glu Lys
 65 70 75 80
 Val Lys Pro Gln Cys Lys Glu Val His Gln Thr Leu Ile Leu Asp Pro
 85 90 95
 Ala Gln Arg Lys Arg Leu Gln Gln Gln Met Gln Gln His Val Gln Leu
 100 105 110
 Leu Thr Gln Ile His Leu Leu Ala Thr Cys Asn Pro Asn Leu Asn Pro
 115 120 125
 Glu Ala Ser Ser Thr Arg Ile Cys Leu Lys Glu Leu Gly Thr Phe Ala
 130 135 140
 Gln Ser Ser Ile Ala Leu His His Gln Tyr Asn Pro Lys Phe Gln Thr
 145 150 155 160
 Leu Phe Gln Pro Cys Asn Leu Met Gly Ala Met Gln Leu Ile Glu Asp
 165 170 175
 Phe Ser Thr His Val Ser Ile Asp Cys Ser Pro His Lys Thr Val Lys
 180 185 190
 Lys Thr Ala Asn Glu Phe Pro Cys Leu Pro Lys Gln Val Ala Trp Ile
 195 200 205
 Leu Ala Thr Ser Lys Val Phe Met Tyr Pro Glu Leu Leu Pro Val Cys
 210 215 220
 Ser Leu Lys Ala Lys Asn Pro Gln Asp Lys Ile Leu Phe Thr Lys Ala
 225 230 235 240
 Glu Asp Asn Leu Leu Ala Leu Gly Leu Lys His Phe Glu Gly Thr Glu
 245 250 255
 Phe Leu Asn Pro Leu Ile Ser Lys Tyr Leu Leu Thr Cys Lys Thr Ala
 260 265 270
 Arg Gln Leu Thr Val Arg Ile Lys Asn Leu Asn Met Asn Arg Ala Pro
 275 280 285
 Asp Asn Ile Ile Lys Phe Tyr Lys Lys Thr Lys Gln Leu Pro Val Leu
 290 295 300
 Gly Lys Cys Cys Glu Glu Ile Gln Pro His Gln Trp Lys Pro Pro Ile
 305 310 315 320
 Glu Arg Glu Glu His Arg Leu Pro Phe Trp Leu Lys Ala Ser Leu Pro
 325 330 335
 Ser Ile Gln Glu Glu Leu Arg His Met Ala Asp Gly Ala Arg Glu Val
 340 345 350
 Gly Asn Met Thr Gly Thr Thr Glu Ile Asn Ser Asp Gln Gly Leu Glu
 355 360 365

Lys Asp Asn Ser Glu Leu Gly Ser Glu Thr Arg Tyr Pro Leu Leu Leu
 370 375 380
 Pro Lys Gly Val Val Leu Lys Leu Lys Pro Val Ala Asp Arg Phe Pro
 385 390 395 400
 Lys Lys Ala Trp Arg Gln Lys Arg Ser Ser Val Leu Lys Pro Leu Leu
 405 410 415
 Ile Gln Pro Ser Pro Ser Leu Gln Pro Ser Phe Asn Pro Gly Lys Thr
 420 425 430
 Pro Ala Gln Ser Thr His Ser Glu Ala Pro Pro Ser Lys Met Val Leu
 435 440 445
 Arg Ile Pro His Pro Ile Gln Pro Ala Thr Val Leu Gln Thr Val Pro
 450 455 460
 Gly Val Pro Pro Leu Gly Val Ser Gly Gly Glu Ser Phe Glu Ser Pro
 465 470 475 480
 Ala Ala Leu Pro Ala Met Pro Pro Glu Ala Arg Thr Ser Phe Pro Leu
 485 490 495
 Ser Glu Ser Gln Thr Leu Leu Ser Ser Ala Pro Val Pro Lys Val Met
 500 505 510
 Met Pro Ser Pro Ala Ser Ser Met Phe Arg Lys Pro Tyr Val Arg Arg
 515 520 525
 Arg Pro Ser Lys Arg Arg Gly Ala Arg Ala Phe Arg Cys Ile Lys Pro
 530 535 540
 Ala Pro Val Ile His Pro Ala Ser Val Ile Phe Thr Val Pro Ala Thr
 545 550 555 560
 Thr Val Lys Ile Val Ser Leu Gly Gly Gly Cys Asn Met Ile Gln Pro
 565 570 575
 Val Asn Ala Ala Val Ala Gln Ser Pro Gln Thr Ile Pro Ile Ala Thr
 580 585 590
 Leu Leu Val Asn Pro Thr Ser Phe Pro Cys Pro Leu Asn Gln Pro Leu
 595 600 605
 Val Ala Ser Ser Val Ser Pro Leu Ile Val Ser Gly Asn Ser Val Asn
 610 615 620
 Leu Pro Ile Pro Ser Thr Pro Glu Asp Lys Ala His Met Asn Val Asp
 625 630 635 640
 Ile Ala Cys Ala Val Ala Asp Gly Glu Asn Ala Phe Gln Gly Leu Glu
 645 650 655
 Pro Lys Leu Glu Pro Gln Glu Leu Ser Pro Leu Ser Ala Thr Val Phe
 660 665 670
 Pro Lys Val Glu His Ser Pro Gly Pro Pro Pro Val Asp Lys Gln Cys
 675 680 685

Gln Glu Gly Leu Ser Glu Asn Ser Ala Tyr Arg Trp Thr Val Val Lys
690 695 700

Thr Glu Glu Gly Arg Gln Ala Leu Glu Pro Leu Pro Gln Gly Ile Gln
705 710 715 720

Glu Ser Leu Asn Asn Ser Ser Pro Gly Asp Leu Glu Glu Val Val Lys
725 730 735

Met Glu Pro Glu Asp Ala Thr Glu Glu Ile Ser Gly Phe Leu
740 745 750

<210> 127

<211> 2673

<212> DNA

<213> Homo sapiens

<400> 127

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gaagaggaag aaccaatgga tacttccagt gtaactcaca cagaacacta caagacactg 180
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<210> 128

<211> 633

<212> PRT

<213> Homo sapiens

<400> 128

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 Glu Pro Met Asp Thr Ser Ser Val Thr His Thr Glu His Tyr Lys Thr
 20 25 30
 Leu Ile Glu Ala Gly Leu Pro Gln Lys Val Ala Glu Arg Leu Asp Glu
 35 40 45
 Ile Phe Gln Thr Gly Leu Val Ala Tyr Val Asp Leu Asp Glu Arg Ala
 50 55 60
 Ile Asp Ala Leu Arg Glu Phe Asn Glu Glu Gly Ala Leu Ser Val Leu
 65 70 75 80
 Gln Gln Phe Lys Glu Ser Asp Leu Ser His Val Gln Asn Lys Ser Ala
 85 90 95
 Phe Leu Cys Gly Val Met Lys Thr Tyr Arg Gln Arg Glu Lys Gln Gly
 100 105 110
 Ser Lys Val Gln Glu Ser Thr Lys Gly Pro Asp Glu Ala Lys Ile Lys
 115 120 125
 Ala Leu Leu Glu Arg Thr Gly Tyr Thr Leu Asp Val Thr Thr Gly Gln
 130 135 140
 Arg Lys Tyr Gly Gly Pro Pro Pro Asp Ser Val Tyr Ser Gly Val Gln
 145 150 155 160
 Pro Gly Ile Gly Thr Glu Val Phe Val Gly Lys Ile Pro Arg Asp Leu
 165 170 175
 Tyr Glu Asp Glu Leu Val Pro Leu Phe Glu Lys Ala Gly Pro Ile Trp
 180 185 190
 Asp Leu Arg Leu Met Met Asp Pro Leu Ser Gly Gln Asn Arg Gly Tyr
 195 200 205
 Ala Phe Ile Thr Phe Cys Gly Lys Glu Ala Ala Gln Glu Ala Val Lys
 210 215 220
 Leu Cys Asp Ser Tyr Glu Ile Arg Pro Gly Lys His Leu Gly Val Cys
 225 230 235 240
 Ile Ser Val Ala Asn Asn Arg Leu Phe Val Gly Ser Ile Pro Lys Asn
 245 250 255

Lys Thr Lys Glu Asn Ile Leu Glu Glu Phe Ser Lys Val Thr Glu Gly
 260 265 270
 Leu Val Asp Val Ile Leu Tyr His Gln Pro Asp Asp Lys Lys Lys Asn
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 Arg Gly Phe Cys Phe Leu Glu Tyr Glu Asp His Lys Ser Ala Ala Gln
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 Ala Arg Arg Arg Leu Met Ser Gly Lys Val Lys Val Trp Gly Asn Val
 305 310 315 320
 Val Thr Val Glu Trp Ala Asp Pro Val Glu Glu Pro Asp Pro Glu Val
 325 330 335
 Met Ala Lys Val Lys Val Leu Phe Val Arg Asn Leu Ala Thr Thr Val
 340 345 350
 Thr Glu Glu Ile Leu Glu Lys Ser Phe Ser Glu Phe Gly Lys Leu Glu
 355 360 365
 Arg Val Lys Lys Leu Lys Asp Tyr Ala Phe Val His Phe Glu Asp Arg
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 Gly Ala Ala Val Lys Ala Met Asp Glu Met Asn Gly Lys Glu Ile Glu
 385 390 395 400
 Gly Glu Glu Ile Glu Ile Val Leu Ala Lys Pro Pro Asp Lys Lys Arg
 405 410 415
 Lys Glu Arg Gln Ala Ala Arg Gln Ala Ser Arg Ser Thr Ala Tyr Glu
 420 425 430
 Asp Tyr Tyr Tyr His Pro Pro Pro Arg Met Pro Pro Pro Ile Arg Gly
 435 440 445
 Arg Gly Arg Gly Gly Gly Arg Gly Gly Tyr Gly Tyr Pro Pro Asp Tyr
 450 455 460
 Tyr Gly Tyr Glu Asp Tyr Tyr Asp Asp Tyr Tyr Gly Tyr Asp Tyr His
 465 470 475 480
 Asp Tyr Arg Gly Gly Tyr Glu Asp Pro Tyr Tyr Gly Tyr Asp Asp Gly
 485 490 495
 Tyr Ala Val Arg Gly Arg Gly Gly Gly Arg Gly Gly Arg Gly Ala Pro
 500 505 510
 Pro Pro Pro Arg Gly Arg Gly Ala Pro Pro Pro Arg Gly Arg Ala Gly
 515 520 525
 Tyr Ser Gln Arg Gly Ala Pro Leu Gly Pro Pro Arg Gly Ser Arg Gly
 530 535 540
 Gly Arg Gly Gly Pro Ala Gln Gln Gln Arg Gly Arg Gly Ser Arg Gly
 545 550 555 560
 Ser Arg Gly Asn Arg Gly Gly Asn Val Gly Gly Lys Arg Lys Ala Asp
 565 570 575

Gly Tyr Asn Gln Pro Asp Ser Lys Arg Arg Gln Thr Asn Asn Gln Gln
580 585 590

Asn Trp Gly Ser Gln Pro Ile Ala Gln Gln Pro Leu Gln Gln Gly Gly
595 600 605

Asp Tyr Ser Gly Asn Tyr Gly Tyr Asn Asn Asp Asn Gln Glu Phe Tyr
610 615 620

Gln Asp Thr Tyr Gly Gln Gln Trp Lys
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<210> 129

<211> 938

<212> DNA

<213> Homo sapiens

<400> 129

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<210> 130

<211> 244

<212> PRT

<213> Homo sapiens

<400> 130

Met Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser
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Pro Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys
35 40 45

Lys Leu Glu Gln Leu Tyr Asn Arg Tyr Gln Asp Pro Gln Asp Glu Asn
50 55 60

Lys Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu
65 70 75 80

Asp Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala
85 90 95

Ala Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr
 100 105 110

Glu Leu Gly Cys Asp Ser Ile Glu Lys Leu Lys Ala Gln Ile Pro Lys
 115 120 125

Met Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln
 130 135 140

Phe Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu
 145 150 155 160

Glu Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Lys
 165 170 175

Phe Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His Lys Arg Ser
 180 185 190

Ile Pro Lys Asp Thr Trp Asn Leu Leu Leu Asp Phe Ser Thr Met Ile
 195 200 205

Ala Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Phe
 210 215 220

Ile Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys
 225 230 235 240

Ser Thr Thr Val

<210> 131

<211> 5170

<212> DNA

<213> Homo sapiens

<400> 131

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<210> 132

<211> 695

<212> PRT

<213> Homo sapiens

<400> 132

Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
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 20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
 35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
 65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
 85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
 100 105 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
 115 120 125

Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Arg Cys
 180 185 190

Pro Met Arg Ser Leu Gly Ala Asn Pro Trp Tyr Cys Gly Asp Pro Ala
 195 200 205

Arg Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys Glu
 210 215 220

Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val Cys
 225 230 235 240

Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr Glu
 245 250 255

Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro Ala

260	265	270
Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr Pro 275 280 285		
Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala Pro 290 295 300		
Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg Pro 305 310 315 320		
Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala Asn 325 330 335		
Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly Ser 340 345 350		
Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala Asp 355 360 365		
Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp Asn 370 375 380		
Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn Leu 385 390 395 400		
Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn Asn 405 410 415		
Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser Asn 420 425 430		
Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn Leu 435 440 445		
Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro Gly 450 455 460		
Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn Asn 465 470 475 480		
Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu Ser 485 490 495		
Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala Gly 500 505 510		
Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly Asn 515 520 525		
Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala Glu 530 535 540		
Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr Pro 545 550 555 560		
Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu Ile 565 570 575		
Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His Ser		

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<210> 133
<211> 1564
<212> DNA
<213> Homo sapiens
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<210> 134
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<212> PRT

<213> Homo sapiens

<400> 134

Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser Val
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Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu Asp Leu
 20 25 30

Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly Thr Arg Thr
 35 40 45

Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly Thr Ala Ser Pro
 50 55 60

Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro Thr Val Ser Arg Leu
 65 70 75 80

Glu Ala Leu Thr Arg Ala Val Gln Val Ala Glu Pro Leu Gly Ser Cys
 85 90 95

Gly Phe Gln Gly Gly Pro Cys Pro Gly Arg Arg Arg Asp
 100 105

<210> 135

<211> 839

<212> DNA

<213> Homo sapiens

<400> 135

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 acagggtttt ttcttagttt gttgcctaag agtacaccaa atgtgacatc ctttcaccaa 180
 tatagattac ttcataccac attgtcaagg aaaggactag aagaattttt tgatgaccca 240
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<210> 136

<211> 250

<212> PRT

<213> Homo sapiens

<400> 136

Met Ala Ala Ala Gly Leu Ala Leu Leu Cys Arg Arg Val Ser Ser Ala
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Leu Lys Ser Ser Arg Ser Leu Ile Thr Pro Gln Val Pro Ala Cys Thr
 20 25 30

Gly Phe Phe Leu Ser Leu Leu Pro Lys Ser Thr Pro Asn Val Thr Ser

35 40 45
 Phe His Gln Tyr Arg Leu Leu His Thr Thr Leu Ser Arg Lys Gly Leu
 50 55 60
 Glu Glu Phe Phe Asp Asp Pro Lys Asn Trp Gly Gln Glu Lys Val Lys
 65 70 75 80
 Ser Gly Ala Ala Trp Thr Cys Gln Gln Leu Arg Asn Lys Ser Asn Glu
 85 90 95
 Asp Leu His Lys Leu Trp Tyr Val Leu Leu Lys Glu Arg Asn Met Leu
 100 105 110
 Leu Thr Leu Glu Gln Glu Ala Lys Arg Gln Arg Leu Pro Met Pro Ser
 115 120 125
 Pro Glu Arg Leu Asp Lys Val Val Asp Ser Met Asp Ala Leu Asp Lys
 130 135 140
 Val Val Gln Glu Arg Glu Asp Ala Leu Arg Leu Leu Gln Thr Gly Gln
 145 150 155 160
 Glu Arg Ala Arg Pro Gly Ala Trp Arg Arg Asp Ile Phe Gly Arg Ile
 165 170 175
 Ile Trp His Lys Phe Lys Gln Trp Val Ile Pro Trp His Leu Asn Lys
 180 185 190
 Arg Tyr Asn Arg Lys Arg Phe Phe Ala Leu Pro Tyr Val Asp His Phe
 195 200 205
 Leu Arg Leu Glu Arg Glu Lys Arg Ala Arg Ile Lys Ala Arg Lys Glu
 210 215 220
 Asn Leu Glu Arg Lys Lys Ala Lys Ile Leu Leu Lys Lys Phe Pro His
 225 230 235 240
 Leu Ala Glu Ala Gln Lys Ser Ser Leu Val
 245 250

<210> 137

<211> 1067

<212> DNA

<213> Homo sapiens

<400> 137

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<210> 138

<211> 189

<212> PRT

<213> Homo sapiens

<400> 138

Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Pro Trp Thr
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 Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
 20 25 30
 Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His
 35 40 45
 Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr
 50 55 60
 Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln
 65 70 75 80
 Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly
 85 90 95
 Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu
 100 105 110
 Pro Ser Leu Leu Pro Asp Ser Pro Val Gly Gln Leu His Ala Ser Leu
 115 120 125
 Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr
 130 135 140
 Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu
 145 150 155 160
 Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala
 165 170 175
 Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro
 180 185

<210> 139

<211> 1785

<212> DNA

<213> Homo sapiens

<400> 139

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 gaaaagacag ggaaaaaaat tctaagatac atgaatccca gaccattgct ctccaaatat 180
 tttcaagtga ttcattctct ttatttaaaa aatgaattaa ccaccagatg ggacactcat 240

```

acattcctga tggttgtagg aatcagtaga ccctgtatgg aaagcaatag gataaatattt 300
cataggatca aattaaaatg ttcacagcat tggttccagg aaattggcctt ctggagaatt 360
tatactccag aaacaattca acaaaagaac acagctctgt gcatgcagat gctcattagc 420
ccatcaccta gagtaaggga aagtggagat cccaatgaac aacaatgaga tgggttagcg 480
aactgtgacc tatcagccca atggacattt aagcaatcac tgaaaagtag aaacatgaag 540
atattacaca acatgaaaac tgtttatgga gtatatattag gtaaaaagga aaaaaaggca 600
gaactgtata tctgtggttg gatatacttt ttttttttaa tattaagcac caaccaaag 660
aagaaaaggag gatagaaaaa ataaaatgga agatgtaggg tgggcagatt agggctgcgt 720
ttgttgcttg ctttcatggt accatcatag cgtttttgcc acttacaag gaggaaaaaa 780
atcaattctg tgccaaccca gacaacagag acctgagtgg ggggtgggaa gagagatttt 840
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atatgtatc ttaccaggcc cactcagaga aacagcactt atctttaaaa ttatttttta 1680
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```

<210> 140

<211> 86

<212> PRT

<213> Homo sapiens

<400> 140

```

Met Gly Ala Phe Val Leu Arg Gly Arg Gly Thr Ser Leu Glu Gly Ala
  1                   5                   10                   15

```

```

Gly Ala Lys Gly Lys Cys Ile Ser Arg Thr Gly Gly Phe Ile Ile Pro
      20                   25                   30

```

```

Ser Val Ser Asp Arg Met Val Thr Glu Ala Leu Trp Thr Tyr Phe Pro
      35                   40                   45

```

```

Ala Phe Ser Ser His Gln Gly Trp Val Cys Thr Gly Gly Lys Gly Pro
      50                   55                   60

```

```

Gln Glu Glu Ala Leu Ile Phe Asn Lys Thr Cys Phe Leu Arg Thr Ala
      65                   70                   75                   80

```

```

Asn Lys Arg Lys Ala Gln
      85

```

<210> 141

<211> 947

<212> DNA

<213> Homo sapiens

<400> 141

```

caaactgaag gtaggatgtc tatataccct tcatttcagg ggcccctaga gaatatacct 60
tagctttccc tcttcggca tcttgaaaag tggatacctg tggccttctt ttcactttga 120

```

```

aagcttacac cctcattttg actacaacta atactaaaag cttggcatct tgcttgagat 180
tagtgtttgc tatgccaaac accttctcct ctttctattg aaagcaaaac ataggaaaat 240
aatttgaaat acttttaagg catcttaaaa acatgacttt ttcattctat ggaaaagcag 300
accaattttg cttttttttc ccaacttggt ctcagactg tgccaataaa atgtgttcat 360
agcaggaaaa tttggaaaat acagaaaagc actatgaaga aaacaaaatg tacccaaaat 420
cccacactc agataacatc actgttaatg ttttgatatg tatttccagt cttttctatt 480
gtgttaattt ttcattttgt ttttgaataa ataactttca ggaaagaaat tgagcctttt 540
ctgccacctc tgaagcctga ttactgtgtg aagcaggcca tgaaggccat cctcactgac 600
cagcccatga tctgcactcc ccgcctcatg tacatcgtga ctttcatgaa gagcatccta 660
ccatttgaag cagttgtgtg catgtatcgg ttcctaggag cggacaagtg tatgtacccc 720
tttattgtc aaagaagca agccacaaac aataatgaag caaaaaatg aatctaagaa 780
tctttttgta tggaatatta cttctatcag aagatgatca agatgtttca gtccagtgc 840
catcagcatt gctgacattt tatggattct aaacttgtgt tgtttctttt ttaaatcaac 900
tttttaaaaa aataaagtgt aaattaaccg acaaaaaaaaa aaaaaaa 947

```

<210> 142

<211> 65

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Lys Ala Ile Leu Thr Asp Gln Pro Met Ile Cys Thr Pro Arg Leu
  1             5             10             15

```

```

Met Tyr Ile Val Thr Phe Met Lys Ser Ile Leu Pro Phe Glu Ala Val
          20             25             30

```

```

Val Cys Met Tyr Arg Phe Leu Gly Ala Asp Lys Cys Met Tyr Pro Phe
          35             40             45

```

```

Ile Ala Gln Arg Lys Gln Ala Thr Asn Asn Asn Glu Ala Lys Asn Gly
          50             55             60

```

Ile

65

<210> 143

<211> 1148

<212> DNA

<213> Homo sapiens

<400> 143

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gcgagatccc taccgcagta tccgcctctg ccgcgcgcca gcttcccga cctcttcagc 60
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gcccgcgccc cgagcccgcc gccgccttc gagggcgccc caggccgcg catggtgaag 180
gtgacgttca actccgctct ggcccagaag gaggccaaga aggacgagcc caagagcggc 240
gaggaggcgc tcatcatccc ccccgacgcc gtcgcggtgg actgcaagga cccagatgat 300
gtggtaccag ttggccaaag aagagcctgg tgttggtgca tgtgctttgg actagcattt 360
atgcttgacg gtgttattct aggaggagca tacttgtaca aatattttgc acttcaacca 420
gatgacgtgt actactgtgg aataaagtac atcaaagatg atgtcatctt aaatgagccc 480
tctgcagatg cccagctgc tctctaccag acaattgaag aaaatattaa aatctttgaa 540
gaagaagaag ttgaatttat cagtgtgcct gtcccagagt ttgcagatag tgatcctgcc 600
aacattgttc atgactttta caagaaactt acagcctatt tagatcttaa cctggataag 660
tgctatgtga tcctctgaa cacttccatt gttatgccac ccagaaacct actggagtta 720
cttattaaca tcaaggctgg aacctatttg cctcagtcct atctgattca tgagcacatg 780
gttattactg atcgatttga aaacattgat cacctgggtt tctttattta tcgactgtgt 840
catgacaagg aaacttacaa actgcaacgc agagaaacta ttaaaggat tcagaaacct 900
gaagccagca attgtttcgc aattcggcat tttgaaaaca aatttgcgt ggaaacttta 960
atttgttctt gaacagtcaa gaaaaacatt attgaggaaa attaatatca cagcataacc 1020

```

ccacccttta cattttgtgc agtgattatt ttttaaagtc ttctttcatg taagtagcaa 1080
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 aaaaaaaaa 1148

<210> 144

<211> 266

<212> PRT

<213> Homo sapiens

<400> 144

Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys Glu Ala Lys
 1 5 10 15
 Lys Asp Glu Pro Lys Ser Gly Glu Glu Ala Leu Ile Ile Pro Pro Asp
 20 25 30
 Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro Val Gly
 35 40 45
 Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala Phe Met
 50 55 60
 Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr Phe Ala
 65 70 75 80
 Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile Lys Asp
 85 90 95
 Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala Leu Tyr
 100 105 110
 Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Glu Val Glu
 115 120 125
 Phe Ile Ser Val Pro Val Pro Glu Phe Ala Asp Ser Asp Pro Ala Asn
 130 135 140
 Ile Val His Asp Phe Asn Lys Lys Leu Thr Ala Tyr Leu Asp Leu Asn
 145 150 155 160
 Leu Asp Lys Cys Tyr Val Ile Pro Leu Asn Thr Ser Ile Val Met Pro
 165 170 175
 Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly Thr Tyr
 180 185 190
 Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr Asp Arg
 195 200 205
 Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu Cys His
 210 215 220
 Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys Gly Ile
 225 230 235 240
 Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe Glu Asn
 245 250 255
 Lys Phe Ala Val Glu Thr Leu Ile Cys Ser
 260 265

<210> 145
 <211> 1353
 <212> DNA
 <213> Homo sapiens

<400> 145
 aggtctagaa ttcaatcggc cgcttttttt ttttttttt ttgctaacac ccagttctgc 60
 ctgctacacc acctgggaat tgaccatcca gctgtgttct ctctgcctct ggcccagtag 120
 caactgacct gccctattcc tggctgatct catgctgctg aagttcaagg cgctggacac 180
 actaccctga tttttgttgc acctggccta gctcatttaa cttggcaatt agttggtggt 240
 tttctttctt tcttcttctt ttttttttta attcatttca tttctgtcac cctttaattt 300
 tcattcttct tttttaagta gttgttccat gctgtgtttt tttgttttat ctttcattgc 360
 ctttcctctt gcagtcaaca ttatgacctg gggactccag catccttcaa gcaagccatt 420
 tccgaagaag gtgaaaagaa gccaggatga ttggcacctc ctctcctcc tctcttctt 480
 cctcttcctt tgcccagccc cctcctgtgc gtgtgtttca gacaacacag gagccagcac 540
 aggagtggaa aatcctgcag cgcaactcag ctcagcccac agaagccttg ggaatggcct 600
 cagtttgtgc aataagaaga tttttttttt ctttttaaat cttcattata ttttctttga 660
 ttgtctgtga gaaagtaccc aggtccgcct ggaattactc tacagtagaa ataactgaac 720
 acaacaacac tgatggaaaa aaagagttaa ctattttatt tatttcaata tttaaaagga 780
 aaaaagtgtc gacatggcac agtatttttg tttaaagtac ctctacttc aaaagttaag 840
 cgcaattttg tgaagacatg aaatcataag agtacttaat gtaaaataaa agactgcata 900
 ttaactctaa agaaaaatgc cccacatttt aaataagaaa ataaagatca actctgctct 960
 ctcaggcttt ttaaaaagcc attcatgtat gtgctttagg tatttttatt tctgaggtt 1020
 ggatgtggta agtgaggagt gctcagtttt ttttcctcc ttcaaaagtc tattgaaagt 1080
 gttggtgatg ttaaatgatt gtgtgttaag atttgactga aataacttag ccacaaatca 1140
 gcagtttccc ccaccctcat tgcccctca cccaggcaa gcccctttta tctgaatgtc 1200
 agaagcagcc tgccctctag ttatcatgtc tgatgaggtc tagctcagga aggaattcca 1260
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 aaataatgca gcaaaaaaaa aaaaaaaaaa aaa 1353

<210> 146
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 146
 Met Leu Leu Phe Phe Val Leu Ser Phe Ile Ala Phe Pro Ser Ala Val
 1 5 10 15
 Asn Ile Met Thr Trp Gly Leu Gln His Pro Ser Ser Lys Pro Phe Pro
 20 25 30
 Lys Lys Val Lys Arg Ser Gln Asp Asp Trp His Leu Leu Leu Leu
 35 40 45
 Leu Phe Phe Leu Phe Pro Cys Pro Ala Pro Ser Cys Ala Cys Val Ser
 50 55 60
 Asp Asn Thr Gly Ala Ser Thr Gly Val Glu Asn Pro Ala Ala Gln Leu
 65 70 75 80
 Ser Ser Ala His Arg Ser Leu Gly Asn Gly Leu Ser Leu Cys Asn Lys
 85 90 95
 Lys Ile Phe Phe Phe Phe Leu Asn Leu His Tyr Ile Phe Phe Asp Cys
 100 105 110
 Leu

<210> 147
<211> 2312
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (2224)

<220>
<221> unsure
<222> (2236)

<400> 147
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cccgctccca agcgcgcccc gagcagcccc gtggctaagc cgggtcctgt caagacgctc 180
actcgggaaga aaaacaagaa gaaaaaaagg ttttgaaaaa gcaaggcgcg ggaagtaagc 240
aagaagccag caagcgcccc cggtgctgtg gtgcgacctc caaaggcacc agaagacttt 300
tctcaaaact ggaaggcgct gcaagagtgg ctgctgaaac aaaaatctca ggccccagaa 360
aagcctcttg tcatctctca gatgggttcc aaaaagaagc ccaaaattat ccagcaaaac 420
aaaaaagaga cctcgccctca agtgaaggga gaggagatgc cggcaggaaa agaccaggag 480
gccagcaggg gctctgttcc ttcagggttcc aagatggaca ggaggcgcc agtacctcgc 540
accaaggcca gtggaacaga gcacaataag aaaggaacca aggaaaggac aaatggtgat 600
attgttccag aacgagggga catcgagcat aagaagcgga aagctaagga ggcagcccca 660
gccccacca ccgaggaaga catctggttt gacgacgtgg acccagcgga tatcgaagct 720
gccataggtc cagagcgggc caagatagcg aggaacaggt tgggtcagag cgagggcagc 780
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acggactata ggacagcggt cagtggtgatt cggcctgaga acctcaagca gggagaagag 1020
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gcacaacagg tgttacatca ggggtttcct gtggccgttt gaactttgag catttatcta 1920
aattaaattg gccagggtt ggctgggtggg tcaccagca gaggtcttc cccatagcac 1980
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ggacggagtc caaggcgcta ttgggccacc tgacagctgg acagaaaagg ggcagacaca 2220
ccnggatgc gatttnaaat aaatgcagat gtttacttgg aaaaaaaaaa aaaaaaaaaa 2280
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2312

<210> 148
<211> 422
<212> PRT

<213> Homo sapiens

<400> 148

Met Gly Lys Ala Lys Val Pro Ala Ser Lys Arg Ala Pro Ser Ser Pro
 1 5 10 15
 Val Ala Lys Pro Gly Pro Val Lys Thr Leu Thr Arg Lys Lys Asn Lys
 20 25 30
 Lys Lys Lys Arg Phe Trp Lys Ser Lys Ala Arg Glu Val Ser Lys Lys
 35 40 45
 Pro Ala Ser Gly Pro Gly Ala Val Val Arg Pro Pro Lys Ala Pro Glu
 50 55 60
 Asp Phe Ser Gln Asn Trp Lys Ala Leu Gln Glu Trp Leu Leu Lys Gln
 65 70 75 80
 Lys Ser Gln Ala Pro Glu Lys Pro Leu Val Ile Ser Gln Met Gly Ser
 85 90 95
 Lys Lys Lys Pro Lys Ile Ile Gln Gln Asn Lys Lys Glu Thr Ser Pro
 100 105 110
 Gln Val Lys Gly Glu Glu Met Pro Ala Gly Lys Asp Gln Glu Ala Ser
 115 120 125
 Arg Gly Ser Val Pro Ser Gly Ser Lys Met Asp Arg Arg Ala Pro Val
 130 135 140
 Pro Arg Thr Lys Ala Ser Gly Thr Glu His Asn Lys Lys Gly Thr Lys
 145 150 155 160
 Glu Arg Thr Asn Gly Asp Ile Val Pro Glu Arg Gly Asp Ile Glu His
 165 170 175
 Lys Lys Arg Lys Ala Lys Glu Ala Ala Pro Ala Pro Pro Thr Glu Glu
 180 185 190
 Asp Ile Trp Phe Asp Asp Val Asp Pro Ala Asp Ile Glu Ala Ala Ile
 195 200 205
 Gly Pro Glu Ala Ala Lys Ile Ala Arg Lys Gln Leu Gly Gln Ser Glu
 210 215 220
 Gly Ser Val Ser Leu Ser Leu Val Lys Glu Gln Ala Phe Gly Gly Leu
 225 230 235 240
 Thr Arg Ala Leu Ala Leu Asp Cys Glu Met Val Gly Val Gly Pro Lys
 245 250 255
 Gly Glu Glu Ser Met Ala Ala Arg Val Ser Ile Val Asn Gln Tyr Gly
 260 265 270
 Lys Cys Val Tyr Asp Lys Tyr Val Lys Pro Thr Glu Pro Val Thr Asp
 275 280 285
 Tyr Arg Thr Ala Val Ser Gly Ile Arg Pro Glu Asn Leu Lys Gln Gly
 290 295 300

Glu Glu Leu Glu Val Val Gln Lys Glu Val Ala Glu Met Leu Lys Gly
 305 310 315 320
 Arg Ile Leu Val Gly His Ala Leu His Asn Asp Leu Lys Val Leu Phe
 325 330 335
 Leu Asp His Pro Lys Lys Lys Ile Arg Asp Thr Gln Lys Tyr Lys Pro
 340 345 350
 Phe Lys Ser Gln Val Lys Ser Gly Arg Pro Ser Leu Arg Leu Leu Ser
 355 360 365
 Glu Lys Ile Leu Gly Leu Gln Val Gln Gln Ala Glu His Cys Ser Ile
 370 375 380
 Gln Asp Ala Gln Ala Ala Met Arg Leu Tyr Val Met Val Lys Lys Glu
 385 390 395 400
 Trp Glu Ser Met Ala Arg Asp Arg Arg Pro Leu Leu Thr Ala Pro Asp
 405 410 415
 His Cys Ser Asp Asp Ala
 420

<210> 149

<211> 2103

<212> DNA

<213> Homo sapiens

<400> 149

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 gcttcaggga tcttgagatc cggagcagcc ggggtcggag cggctcctca agagttactg 180
 atctatgaaa tggcagagaa tggaaaaaat tgtgaccaga gacgtgtagc aatgaacaag 240
 gaacatcata atggaaattt cacagacccc tcttcagtga atgaaaagaa gaggaggagg 300
 cgggaagaaa ggcagaatat tgtcctgtgg agacagccgc tcattacctt gcagtatttt 360
 tctctggaaa tccttgtaat ctggaaggaa tggacctcaa aattatggca tcgtcaaagc 420
 attgtggtgt cttttttact gctgcttgc gtgcttatag ctacgtatta tgttgaagga 480
 gtgcatcaac agtatgtgca acgtatagag aaacagtttc ttttgtatgc ctactggata 540
 ggcttaggaa ttttgtcttc tgttgggctt ggaacagggc tgcacacctt tctgctttat 600
 ctgggtccac atatagcctc agttacatta gctgcttatg aatgcaattc agttaatttt 660
 cccgaaccac cctatcctga tcagattatt tgtccagatg aagagggcac tgaaggaacc 720
 atttctttgt ggagtatcat ctcaaaagtt aggattgaag cctgcatgtg gggatatcgg 780
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 gaaccagatg atgaagagta tcaggaattt gaagagatgc tggaaacatgc agagtctgca 900
 caagactttg cctcccgggc caaactggca gttcaaaaac tagtacagaa agttggattt 960
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 tgtggacact tttctgtacc tttttggacc ttctttggtg caaccctaata tggaaaagca 1080
 ataataaaaa tgcataatcca gaaaattttt gttataataa cattcagcaa gcacatagtg 1140
 gagcaaatgg tggctttcat tgggtgctgtc cccggcatag gtccatctct gcagaagcca 1200
 tttcaggagt acctggaggc tcaacggcag aagcttcacc acaaaagcga aatgggcaca 1260
 ccacaggagg aaaactggtt gtcctggatg tttgaaaagt tgggtcgttg catggtgtgt 1320
 tacttcatcc tatctatcat taactccatg gcacaaagtt atgccaaacg aatccagcag 1380
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 tgacatactt tttccttctg tgctaaggta aggtatccac cctcgatgca atccaccttg 1620
 tgttttctta ggggtggaatg tgatgttcag cagcaaactt gcaacagact ggccttctgt 1680
 ttgttacttt caaaaggccc acatgatata attagagaat tcccaccgca caaaaaaagt 1740


```

tcctaagtat gttaaatatg tcaagctttt taggcttgtc acaaagtatt gctttgtttt 1800
cctaagtcac caaaatgtat ataaattatc tagattggat aacagtcttg catgtttatc 1860
atgttacaat ttaatatcc atcctgcccac acccttcttc tcccatcctc aaaaaagggc 1920
cattttatga tgcattgcac accctctggg gaaattgac tttaaatttt gagacagtat 1980
aaggaaaatc tggttggtgt cttacaagtg agctgacacc attttttatt ctgtgtattt 2040
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aaa
2103

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<210> 150

<211> 406

<212> PRT

<213> Homo sapiens

<400> 150

```

Met Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn
  1             5             10             15

```

```

Lys Glu His His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu
      20             25             30

```

```

Lys Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg
      35             40             45

```

```

Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile
      50             55             60

```

```

Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val
      65             70             75             80

```

```

Ser Phe Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu
      85             90             95

```

```

Gly Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu
      100            105            110

```

```

Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly
      115            120            125

```

```

Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser
      130            135            140

```

```

Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro
      145            150            155            160

```

```

Pro Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly
      165            170            175

```

```

Thr Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys
      180            185            190

```

```

Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met
      195            200            205

```

```

Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr
      210            215            220

```

```

Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe
      225            230            235            240

```

```

Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly

```

245 250 255
 Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp
 260 265 270
 Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe
 275 280 285
 Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln
 290 295 300
 Lys Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met
 305 310 315 320
 Val Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys
 325 330 335
 Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys
 340 345 350
 Ser Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe
 355 360 365
 Glu Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile
 370 375 380
 Asn Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn
 385 390 395 400
 Ser Glu Glu Lys Thr Lys
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<210> 151

<211> 1330

<212> DNA

<213> Homo sapiens

<400> 151

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 ggtgattaat ggatggctga gacagctcct taggtggctt aggcctgccc tgtggagcat 180
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 cctggtgtgc ccagctggg aaacatggct gtcatacatt cacatctgtg gaaaggattg 480
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 aataaattca aaattatgtt ctcatttttt tccttgggaac tcaataactc atttcactgg 1260

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 aaaaaaaaaa 1330

<210> 152
 <211> 245
 <212> PRT
 <213> Homo sapiens

<400> 152

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Ser	Lys	Thr	Cys	Thr	Phe	Ser	Ala	Ala	Met	Thr	Thr	Met	Gln	Gly	Met
			20					25					30		
Glu	Gln	Ala	Met	Pro	Gly	Ala	Gly	Pro	Gly	Val	Pro	Gln	Leu	Gly	Asn
		35					40					45			
Met	Ala	Val	Ile	His	Ser	His	Leu	Trp	Lys	Gly	Leu	Gln	Glu	Lys	Phe
	50					55					60				
Leu	Lys	Gly	Glu	Pro	Lys	Val	Leu	Gly	Val	Val	Gln	Ile	Leu	Thr	Ala
65					70				75						80
Leu	Met	Ser	Leu	Ser	Met	Gly	Ile	Thr	Met	Met	Cys	Met	Ala	Ser	Asn
				85					90					95	
Thr	Tyr	Gly	Ser	Asn	Pro	Ile	Ser	Val	Tyr	Ile	Gly	Tyr	Thr	Ile	Trp
		100						105					110		
Gly	Ser	Val	Met	Phe	Ile	Ile	Ser	Gly	Ser	Leu	Ser	Ile	Ala	Ala	Gly
	115						120					125			
Ile	Arg	Thr	Thr	Lys	Gly	Leu	Val	Arg	Gly	Ser	Leu	Gly	Met	Asn	Ile
	130					135					140				
Thr	Ser	Ser	Val	Leu	Ala	Ala	Ser	Gly	Ile	Leu	Ile	Asn	Thr	Phe	Ser
145				150					155					160	
Leu	Ala	Phe	Tyr	Ser	Phe	His	His	Pro	Tyr	Cys	Asn	Tyr	Tyr	Gly	Asn
			165					170						175	
Ser	Asn	Asn	Cys	His	Gly	Thr	Met	Ser	Ile	Leu	Met	Gly	Leu	Asp	Gly
			180					185					190		
Met	Val	Leu	Leu	Leu	Ser	Val	Leu	Glu	Phe	Cys	Ile	Ala	Val	Ser	Leu
	195						200					205			
Ser	Ala	Phe	Gly	Cys	Lys	Val	Leu	Cys	Cys	Thr	Pro	Gly	Gly	Val	Val
	210					215					220				
Leu	Ile	Leu	Pro	Ser	His	Ser	His	Met	Ala	Glu	Thr	Ala	Ser	Pro	Thr
225					230					235					240
Pro	Leu	Asn	Glu	Val											
				245											

<210> 153
 <211> 1724

<212> DNA

<213> Homo sapiens

<400> 153

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attaaaccac cccaatcat tggaagattt ggaacctcac tgaaaattgg tattgttga 180
ttgccaaatg ttgggaaatc tactttcttc aatgtgttaa ccaatagtca ggcttcagca 240
gaaaacttcc cgttctgcac tattgatcct aatgagagca gagtacctgt gccagatgaa 300
aggtttgact ttctttgtca ataccacaaa ccagcaagca aaattcctgc ctttctaaat 360
gtggtggata ttgctggcct tgtgaaagga gctcacaatg ggcaggccct ggggaatgct 420
tttttatctc atattagtgc ctgtgatggc atctttcatc taacacgtgc ttttgaagat 480
gatgatatca cgcacgttga aggaagtgtg gatcctattc gagatataga aataatacat 540
gaagagcttc agcttaagaa tgaggaaatg attgggcccc ttatagataa actagaaaag 600
gtggctgtga gaggaggaga taaaaaacta aaacctgaat atgatataat gtgcaaagta 660
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gagattgaag tgttgaatac acacttattt ttgacttcaa aaccaatggg ctacttgggt 780
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<210> 154

<211> 396

<212> PRT

<213> Homo sapiens

<400> 154

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Met Pro Pro Lys Lys Gly Gly Asp Gly Ile Lys Pro Pro Pro Ile Ile
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Gly Arg Phe Gly Thr Ser Leu Lys Ile Gly Ile Val Gly Leu Pro Asn
 20             25             30
Val Gly Lys Ser Thr Phe Phe Asn Val Leu Thr Asn Ser Gln Ala Ser
 35             40             45
Ala Glu Asn Phe Pro Phe Cys Thr Ile Asp Pro Asn Glu Ser Arg Val
 50             55             60
Pro Val Pro Asp Glu Arg Phe Asp Phe Leu Cys Gln Tyr His Lys Pro
 65             70             75             80
Ala Ser Lys Ile Pro Ala Phe Leu Asn Val Val Asp Ile Ala Gly Leu
 85             90             95
Val Lys Gly Ala His Asn Gly Gln Gly Leu Gly Asn Ala Phe Leu Ser
100            105            110

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His Ile Ser Ala Cys Asp Gly Ile Phe His Leu Thr Arg Ala Phe Glu
 115 120 125
 Asp Asp Asp Ile Thr His Val Glu Gly Ser Val Asp Pro Ile Arg Asp
 130 135 140
 Ile Glu Ile Ile His Glu Glu Leu Gln Leu Lys Asp Glu Glu Met Ile
 145 150 155 160
 Gly Pro Ile Ile Asp Lys Leu Glu Lys Val Ala Val Arg Gly Gly Asp
 165 170 175
 Lys Lys Leu Lys Pro Glu Tyr Asp Ile Met Cys Lys Val Lys Ser Trp
 180 185 190
 Val Ile Asp Gln Lys Thr Pro Val Arg Phe Tyr His Asp Trp Asn Asp
 195 200 205
 Lys Glu Ile Glu Val Leu Asn Thr His Leu Phe Leu Thr Ser Lys Pro
 210 215 220
 Met Val Tyr Leu Val Asn Leu Ser Glu Lys Asp Tyr Ile Arg Lys Lys
 225 230 235 240
 Asn Lys Trp Leu Ile Lys Ile Lys Glu Trp Val Asp Lys Tyr Asp Pro
 245 250 255
 Gly Ala Leu Val Ile Pro Phe Ser Gly Ala Leu Glu Leu Lys Leu Gln
 260 265 270
 Glu Leu Ser Ala Glu Glu Arg Gln Lys Tyr Leu Glu Ala Asn Met Thr
 275 280 285
 Gln Ser Ala Leu Pro Lys Ile Ile Lys Ala Gly Phe Ala Ala Leu Gln
 290 295 300
 Leu Glu Tyr Phe Phe Thr Ala Gly Pro Asp Glu Val Arg Ala Trp Thr
 305 310 315 320
 Ile Arg Lys Gly Thr Lys Ala Pro Gln Ala Ala Gly Lys Ile His Thr
 325 330 335
 Asp Phe Glu Lys Gly Phe Ile Met Ala Glu Val Met Lys Tyr Glu Asp
 340 345 350
 Phe Lys Glu Glu Gly Ser Glu Asn Ala Val Lys Ala Ala Gly Lys Tyr
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 385 390 395

<210> 155

<211> 2291

<212> DNA

<213> Homo sapiens

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<400> 155
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aggggatttg atgttggtcc actatgaagg ctacttagaa aaggacggct ccttatttca 300
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cattcctcct gctctgggct atggaaaaga aggaaaagggt aaaattcccc cagaaagtac 480
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tacataataa cagcatgagt tatagagata catctaccct tttaatatag cactcatctt 780
tcaagagagg gcagtcattt ttaaagaaca ttttattttt atacaatgct ctttcttgct 840
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<210> 156

<211> 211

<212> PRT

<213> Homo sapiens

<400> 156

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Met Arg Leu Phe Leu Trp Asn Ala Val Leu Thr Leu Phe Val Thr Ser
  1                      5                      10                     15

Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu Val Leu
  20                      25                     30

Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly Asp Leu Met
  35                      40                     45

Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly Ser Leu Phe His
  50                      55                     60

```

Ser Thr His Lys His Asn Asn Gly Gln Pro Ile Trp Phe Thr Leu Gly
 65 70 75 80

Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln Gly Leu Lys Gly Met Cys
 85 90 95

Val Gly Glu Lys Arg Lys Leu Ile Ile Pro Pro Ala Leu Gly Tyr Gly
 100 105 110

Lys Glu Gly Lys Gly Lys Ile Pro Pro Glu Ser Thr Leu Ile Phe Asn
 115 120 125

Ile Asp Leu Leu Glu Ile Arg Asn Gly Pro Arg Ser His Glu Ser Phe
 130 135 140

Gln Glu Met Asp Leu Asn Asp Asp Trp Lys Leu Ser Lys Asp Glu Val
 145 150 155 160

Lys Ala Tyr Leu Lys Lys Glu Phe Glu Lys His Gly Ala Val Val Asn
 165 170 175

Glu Ser His His Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp
 180 185 190

Glu Asp Lys Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His
 195 200 205

Asp Glu Leu
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<210> 157

<211> 2229

<212> DNA

<213> Homo sapiens

<400> 157

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aaaaaaaaa
2229

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<210> 158

<211> 239

<212> PRT

<213> Homo sapiens

<400> 158

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Met Thr Ser Met Pro Ser Glu Lys Gln Asn Val Val Ile Gln Val Val
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Asp Lys Leu Lys Gly Phe Ser Ile Ala Pro Asp Val Cys Glu Thr Thr
      20              25              30

Thr His Val Leu Ser Gly Lys Pro Leu Arg Thr Leu Asn Val Leu Leu
      35              40              45

Gly Ile Ala Arg Gly Cys Trp Val Leu Ser Tyr Asp Trp Val Leu Trp
      50              55              60

Ser Leu Glu Leu Gly His Trp Ile Ser Glu Glu Pro Phe Glu Leu Ser
      65              70              75              80

His His Phe Pro Ala Ala Pro Leu Cys Arg Ser Glu Cys His Leu Ser
      85              90              95

Ala Gly Pro Tyr Arg Gly Thr Leu Phe Ala Asp Gln Pro Ala Met Phe
      100             105             110

Val Ser Pro Ala Ser Ser Pro Pro Val Ala Lys Leu Cys Glu Leu Val
      115             120             125

His Leu Cys Gly Gly Arg Val Ser Gln Val Pro Arg Gln Ala Ser Ile
      130             135             140

Val Ile Gly Pro Tyr Ser Gly Lys Lys Lys Ala Thr Val Lys Tyr Leu
      145             150             155             160

Ser Glu Lys Trp Val Leu Gly Lys Asn Pro Gly Thr Gln Thr Leu Trp
      165             170             175

Cys Gly Pro Asp Leu Trp Thr Gly Phe Gln Gly Gly Arg Arg Gln Ala
      180             185             190

His Thr Pro Phe His Ala Ala Gly Ala Pro Gly Leu Met Ser Gln Pro
      195             200             205

```


Pro Ala Ser Ala Leu Ala Ala Ser Cys Gly His Pro Arg His Ser Arg
 210 215 220

Ser Leu Leu Leu Ala Asp Val Gln Phe Thr Arg Lys Trp Glu Leu
 225 230 235

<210> 159

<211> 3580

<212> DNA

<213> Homo sapiens

<400> 159

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His Gly Arg Phe Gln Trp Thr Leu Tyr Phe Val Leu Gly Leu Ala Leu
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/18298

A. CLASSIFICATION OF SUBJECT MATTER IPC(6) : Please See Extra Sheet. US CL : Please See Extra Sheet. According to International Patent Classification (IPC) or to both national classification and IPC				
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 536/23.1, 23.5; 530/300, 350; 435/69.1, 320.1, 325, 252.3, 254.11; 514/2, 12 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) WEST, MEDLINE search terms: co627, kenneth jacobs				
C. DOCUMENTS CONSIDERED TO BE RELEVANT				
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.		
X, P	WO 98/45436 A2 (GENETICS INSTITUTE, INC.) 15 October 1998, especially SEQ ID NO: 407 on pages 221, and claim 1.	1		
X	Database Medline on Dialog, US National Library of Medicine, (Bethesda, MD, USA) GenBank Accession Number AA287697 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . 'National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index'. 13 August 1997.	1-3		
X	Database Medline on Dialog, US National Library of Medicine, (Bethesda, MD, USA) GenBank Accession Number AA179549. HILLIER et al. 'WashU-Merck EST Project'. 31 December 1996.	1-3		
X	Database Medline on Dialog, US National Library of Medicine, (Bethesda, MD, USA) GenBank Accession Number AA057573. HILLIER et al. 'Generation and analysis of 280,00 human expressed sequence tags'. 02 February 1997.	1-3		
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.				
<table border="0"> <tr> <td> * Special categories of cited documents: *A* document defining the general state of the art which is not considered to be of particular relevance *B* earlier document published on or after the international filing date *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) *O* document referring to an oral disclosure, use, exhibition or other means *P* document published prior to the international filing date but later than the priority date claimed </td> <td> *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art *Z* document member of the same patent family </td> </tr> </table>			* Special categories of cited documents: *A* document defining the general state of the art which is not considered to be of particular relevance *B* earlier document published on or after the international filing date *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) *O* document referring to an oral disclosure, use, exhibition or other means *P* document published prior to the international filing date but later than the priority date claimed	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art *Z* document member of the same patent family
* Special categories of cited documents: *A* document defining the general state of the art which is not considered to be of particular relevance *B* earlier document published on or after the international filing date *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) *O* document referring to an oral disclosure, use, exhibition or other means *P* document published prior to the international filing date but later than the priority date claimed	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art *Z* document member of the same patent family			
Date of the actual completion of the international search 02 NOVEMBER 1999		Date of mailing of the international search report 09 DEC 1999		
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230		Authorized officer CLAIRE M. KAUFMAN Telephone No. (703) 308-0196		

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/18298

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	BOSSY et al. Conservation of neural nicotinic acetylcholine receptors from Drosophila to vertebrate central nervous systems. EMBO J. June 1988, Vol.7, No. 3, pages 611-618, especially Figure 2.	1-7, 9, 11
X,P	Database Medline on Dialog, US National Library of Medicine, (Bethesda, MD, USA) GenBank Accession Number AL035661. SULSTON J. 'Direct Submission'. 15 March 1999.	1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/18298**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-11

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/18298

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

C07K 14/435, 14/00, 7/06; C12N 5/10, 15/10, 15/11, 15/12, 15/63; A61K 38/16

A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

536/23.1, 23.5; 530/300, 350; 435/69.1, 320.1, 325, 252.3, 254.11; 514/2, 12

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-11, drawn to polynucleotide of clone oo62_12, gene, vector, host cell, method of producing a protein and encoded protein.

Group II-LXXIX, each group consisting of two consecutive claims, drawn to polynucleotide of a distinct clone and encoded protein.

The inventions listed as Groups I-LXXIX do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I corresponds to the first invention wherein the first product is the polynucleotide and the first method of using is the method of making the protein. Note there is no method of making the polynucleotide. The invention also includes the protein made. Each group does not share the same or corresponding special technical feature because each group is drawn to a different polynucleotide and encoded protein. This Authority therefore considers that the several inventions do not share a special technical feature within the meaning of PCT Rule 13.2 and thus do not relate to a single general inventive concept within the meaning of PCT Rule 13.1.